

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 76.2887 Seconds  
(without alignments)  
3001.261 Million cell updates/sec

Title: US-09-724-254A-3  
Perfect score: 3124  
Sequence: 1 MLWVILLVLPVSGQPART.....AEFSLTHFKNLPALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3111	99.6	592	4	AAB82314 Human imm
2	3111	99.6	592	7	ADM35236 Human LY1
3	2950	94.4	759	4	AAB82313 Human imm
4	2950	94.4	759	7	ADM35235 Human LY1
5	2950	94.4	977	4	AAB82315 Human imm
6	2950	94.4	977	6	ABP97215 Tumour-as
7	2950	94.4	977	7	ADM35237 Human LY1
8	2918.5	93.4	875	8	ADM82476 Human dia
9	2685.5	86.0	837	8	ADM82477 Human dia
10	1193.5	38.2	582	6	ABU99155 Novel hum
11	1193.5	38.2	582	8	ADM93875 Human NOV
12	1193.5	38.2	707	7	ADM06089 Human pro
13	1193.5	38.2	734	4	AAB82316 Human imm
14	1193.5	38.2	734	7	ADM35238 Human LY1
15	1193.5	38.2	750	8	ADM84916 Human dia
16	1191	38.1	733	8	ADL06557 Human tum
17	1176	37.6	727	6	ABB84668 Human SEC
18	1150.5	36.8	554	7	ADF74336 Extracell
19	1150.5	36.8	717	7	ADF74337 Human FcR
20	1150.5	36.8	717	7	ADF74318 Human FcR
21	1120	35.9	222	5	ABP69283 Human pol
22	1063.5	34.0	718	8	ADM84917 Human dia
23	1031	33.0	707	8	ADM84918 Human dia
24	952.5	30.5	641	8	ADM84919 Human dia
25	900	28.8	181	5	ABP51264 Human MDD

26	900	28.8	181	5	ABP51409 Human MDD
27	889.5	28.5	570	7	ADF74389 Murine Fc
28	889	28.5	468	7	ADF74391 Extracell
29	847.5	27.1	639	7	ADJ70604 Human hea
30	847.5	27.1	655	8	ADM84920 Human dia
31	826.5	26.5	515	4	AAB82312 Human imm
32	826.5	26.5	515	5	ABB80608 Human sbg
33	826.5	26.5	515	7	ADM35234 Human LY1
34	826.5	26.5	515	8	ADP18669 Human pro
35	826	26.4	167	6	ABP75420 Human sec
36	803.5	25.7	421	6	ABU99156 Novel hum
37	803.5	25.7	421	6	ABU99157 Novel hum
38	803.5	25.7	421	8	ADM93877 Human NOV
39	786.5	25.2	421	6	ABU99158 Novel hum
40	786.5	25.2	421	8	ADM93881 Human NOV
41	783.5	25.1	445	7	ADM35268 Human LY1
42	773.5	24.8	508	4	AAB82317 Human imm
43	773.5	24.8	508	7	ADM35239 Human LY1
44	773.5	24.8	508	7	ADM35264 Human LY1
45	773.5	24.8	508	8	ADF89715 Human can

## ALIGNMENTS

RESULT 1  
AAB82314  
ID AAB82314 standard; protein; 592 AA.  
XX  
AC AAB82314;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Human immunoglobulin receptor isoform IRTA2b.  
XX  
KW Immunoglobulin superfamily receptor translocation associated; IRTA;  
KW IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;  
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..15  
FT Protein /label= Signal\_peptide  
FT Protein /label= Mature\_protein  
FT Modified-site 132..134  
FT Modified-site /note= "Asn is N-glycosylated"  
FT Modified-site 383..385  
FT Modified-site /note= "Asn is N-glycosylated"  
WO200138490-A2.  
31-MAY-2001.  
28-NOV-2000; 2000WO-US032403.  
29-NOV-1999; 99US-0168151P.  
(UYCO ) UNIV COLUMBIA NEW YORK.  
Dalla-Favera R;  
WPI; 2001-355921/37.  
N-PSDB; AAP30951.  
XX  
PT New gene encoding immunoglobulin receptor, Immunoglobulin super Receptor  
PT Translocation Associated proteins, used to treat B cell malignancies  
PT including lymphomas and multiple myeloma.  
XX  
PS Claim 3; Fig 18B-1-18B-2; 72pp; English.  
XX  
CC The present sequence is that of the novel human immunoglobulin receptor,

CC immunoglobulin superfamily receptor translocation associated protein  
CC isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of  
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal  
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma  
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding  
CC members of a novel subfamily of related receptors within the  
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA  
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).  
CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at  
CC residue 560, extending for a further 32 residues, whose hydrophobicity  
CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes  
CC display a specific pattern of expression in mature B cells. IRTA2 is  
CC expressed in GC centrocytes and in perifollicular cells, which may  
CC include immunoblasts and memory cells. The invention provides IRTA  
CC nucleic acids and proteins, and antibodies directed to an epitope of an  
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy  
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule  
CC that specifically hybridises with a unique sequence of human IRTA1-5; and  
CC treating a subject having a B cell cancer by administering an anti-IRTA  
CC antibody or an antisense oligonucleotide that specifically hybridises to  
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.  
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
CC Hodgkin's lymphoma  
XX  
SQ Sequence 592 AA;  
  
Query Match 99.6%; Score 3111; DB 4; Length 592;  
Best Local Similarity 99.7%; Pred. No. 3.8e-219; Indels 0; Gaps 0;  
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTFVQGERVTLTKGFRFYSQKTKWYHR 60  
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTFVQGERVTLTKGFRFYSQKTKWYHR 60  
  
Qy 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLLOAPLSVFEQDSVV 120  
Db 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLLOAPLSVFEQDSVV 120  
  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFPHACLKNDNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFPHACLKNDNGAYRCTGYKESCCPVSSNT 180  
  
Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
  
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOQVIPASHPVLTLSPKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOQVIPASHPVLTLSPKALNFE 300  
  
Qy 301 GTKVTLHCETQEDSLRTLYRHYHGVPLRHKSVCRCERGASISFSLTTENSNNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLYRHYHGVPLRHKSVCRCERGASISFSLTTENSNNYCTADNG 360  
  
Qy 361 LGAKPSKAVSLSVTPVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420  
  
Qy 421 LERRANSAGGVAISFSLTAHSGNNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Db 421 LERRANSAGGVAISFSLTAHSGNNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
  
Qy 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPVSGRVSFSLTEGHSNNY 540  
Db 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPVSGRVSFSLTEGHSNNY 540  
  
Qy 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAEFSLTHSKNLFALSSFLP 592  
Db 541 CTADNGFGPQRSEVSLFVTGKCVLASHPPPLAEFSLTHSKNLFALSSFLP 592

RESULT 2  
ADM35236  
ID ADM35236 standard; protein; 592 AA.

XX ADM35236;  
XX 03-JUN-2004 (first entry)  
XX Human LX148P cancer related protein for cancer detection method.  
XX cytostatic; T-cell vaccine; detection; cancer;  
XX chronic lymphocytic leukemia.  
XX Homo sapiens.  
XX WO2003077836-A2.  
XX 25-SEP-2003.  
XX 06-NOV-2002; 2002WO-US035728.  
XX 06-NOV-2001; 2001US-00040862.  
XX 23-MAY-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;  
XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample  
XX from the patient with a binding agent that binds to a cancer-associated  
XX polypeptide and comparing the amount of polypeptide to a predetermined  
XX cutoff value.

XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient  
XX by: (i) contacting a biological sample from the patient with an agent  
XX that binds to any of three polypeptides given in the specification; (ii)  
XX detecting in a sample an amount of the peptide that binds to the binding  
XX agent; and (iii) comparing the amount of polypeptide present in the  
XX patient's sample to a predetermined cutoff value. The specification also  
XX discloses a separate method for detecting (M2) cancer in a patient by a  
XX method similar to M1, except that the detection agent is an  
XX oligonucleotide that binds to any of three polynucleotides given in the  
XX specification. M1 and M2 are useful for detecting the presence of cancer  
XX in a patient, especially chronic lymphocytic leukemia. The applicants  
XX have identified specific human polypeptides overexpressed in one or more  
XX types of hematological malignancies. This sequence corresponds to a  
XX protein used in the method of the invention.

XX Sequence 592 AA;

Query Match 99.6%; Score 3111; DB 7; Length 592;  
Best Local Similarity 99.7%; Pred. No. 3.8e-219; Indels 0; Gaps 0;  
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTFVQGERVTLTKGFRFYSQKTKWYHR 60  
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTFVQGERVTLTKGFRFYSQKTKWYHR 60  
  
Qy 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLLOAPLSVFEQDSVV 120  
Db 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLLOAPLSVFEQDSVV 120  
  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFPHACLKNDNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFPHACLKNDNGAYRCTGYKESCCPVSSNT 180  
  
Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDQTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIOQIPASHPVLTLSPKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIOQIPASHPVLTLSPKALNFE 300  
Qy 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENGNYCTADNG 360  
Db 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSSA 480  
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTGHSGNYY 540  
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTGHSGNYY 540  
Qy 541 CTADNGFGPORSVWSLFTVTKCWLASKPLAEFSLTHSFKNLFASSFLP 592  
Db 541 CTADNGFGPORSVWSLFTVTKCWLASHPPLAEFSLTHSFKNLFASSFLP 592

RESULT 3  
ID AAB82313 standard; protein; 759 AA.  
XX AAB82313;  
AC AAB82313;  
DT 23-JUL-2001 (first entry)  
XX Human immunoglobulin receptor isoform IRTA2a.  
DE Human immunoglobulin receptor translocation associated; IRTA;  
KW IRTA2a; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;  
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..15  
FT /label= signal\_peptide  
FT Protein 16..759  
FT /label= mature\_protein  
FT Modified-site 132..134  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 383..385  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 621..623  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 631..633  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 714..716  
FT /note= "Asn is N-glycosylated"  
XX W0200138490-A2.  
PN 31-MAY-2001.  
XX 28-NOV-2000; 2000WO-US032403.  
XX 29-NOV-1999; 99US-0168151P.  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
PA Dalla-Favera R;  
XX WPI; 2001-355921/37.  
DR

DR N-PSDB; AAF30950.  
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor  
PT Translocation Associated proteins, used to treat B cell malignancies  
PT including lymphomas and multiple myeloma.  
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.  
XX The present sequence is that of the novel human immunoglobulin receptor,  
CC immunoglobulin superfamily receptor translocation associated protein  
CC isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of  
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal  
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma  
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding  
CC members of a novel subfamily of related receptors within the  
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA  
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).  
CC IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains  
CC followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue  
CC 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at  
CC residue 746 and extends for a further 231 residues. The IRTA genes  
CC display a specific pattern of expression in mature B cells. IRTA2 is  
CC expressed in GC centrocytes and in perfollicular cells, which may  
CC include immunoblasts and memory cells. The invention provides IRTA  
CC nucleic acids and proteins, and antibodies directed to an epitope of an  
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy  
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule  
CC that specifically hybridises with a unique sequence of human IRTA1-5; and  
CC treating a subject having a B cell cancer by administering an anti-IRTA  
CC antibody or an antisense oligonucleotide that specifically hybridises to  
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.  
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
CC Hodgkin's lymphoma  
XX  
SQ Sequence 759 AA;  
Query Match 94.4%; Score 2950; DB 4; Length 759;  
Best Local Similarity 98.4%; Pred. No. 3.3e-207;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTFQGERVTLTKGFRFSPQTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPWTTFQGERVTLTKGFRFSPQTKWYHR 60  
Qy 61 YLGKEILRETPDNILEVQSGEYRCQAQGSPLSSPVHLPDSSASLILQAPLSVFEQSVV 120  
Db 61 YLGKEILRETPDNILEVQSGEYRCQAQGSPLSSPVHLPDSSASLILQAPLSVFEQSVV 120  
Qy 121 LRCRAKAEVTLANTTIYKNDNLVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLANTTIYKNDNLVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLCETOLSERSDVPLRFRFRDDQTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIOQIPASHPVLTLSPKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIOQIPASHPVLTLSPKALNFE 300  
Qy 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENGNYCTADNG 360  
Db 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTENGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSSA 480

Db 421 LERRSAGGVAISFSLTAHSGNYICTADNGFGPQSKAVSLIIVPVSHPVLTLSA 480  
QY 481 EALTPEGATVTLHCEVQSGSPQILLYQFYHEDMPLVSSSTPSVGRVSFSLSLTEGHSNGY 540  
Db 481 EALTPEGATVTLHCEVQSGSPQILLYQFYHEDMPLVSSSTPSVGRVSFSLSLTEGHSNGY 540  
QY 541 CTADNGFGPQSEVVSFLVTKCWVLASKPPL 572  
Db 541 CTADNGFGPQSEVVSFLVTKCWVLASKPPL 568

RESULT 4  
ADM35235  
ID ADM35235 standard; protein; 759 AA.  
XX AC ADM35235;  
XX DT 03-JUN-2004 (first entry)  
XX Human LX148P cancer related protein for cancer detection method.  
XX cyostatic; T-cell vaccine; detection; cancer;  
XX chronic lymphocytic leukemia.  
XX Homo sapiens.  
XX WO2003077836-A2.  
XX 25-SEP-2003.  
XX 06-NOV-2002; 2002WO-US035728.  
XX 06-NOV-2001; 2001US-00040862.  
XX 23-MAY-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.  
XX Gaiger A, Algate PA, Mannion J, Retter M;  
XX WPI; 2003-756941/71.  
XX Detecting cancer in a patient comprises contacting a biological sample  
XX from the patient with a binding agent that binds to a cancer-associated  
XX polypeptide and comparing the amount of polypeptide to a predetermined  
XX cutoff value.  
XX Disclosure; SEQ ID NO 10460; 419pp; English.  
XX The invention relates to a method of detecting (M1) cancer in a patient  
XX by: (i) contacting a biological sample from the patient with an agent  
XX that binds to any of three polypeptides given in the specification; (ii)  
XX detecting in a sample an amount of the peptide that binds to the binding  
XX agent; and (iii) comparing the amount of polypeptide present in the  
XX patient's sample to a predetermined cutoff value. The specification also  
XX discloses a separate method for detecting (M2) cancer in a patient by a  
XX method similar to M1, except that the detection agent is an  
XX oligonucleotide that binds to any of three polynucleotides given in the  
XX specification. M1 and M2 are useful for detecting the presence of cancer  
XX in a patient, especially chronic lymphocytic leukemia. The applicants  
XX have identified specific human polypeptides overexpressed in one or more  
XX types of hematological malignancies. This sequence corresponds to a  
XX protein used in the method of the invention.  
XX  
XX Sequence 759 AA;  
Query Match 94.4%; Score 2950; DB 7; Length 759;  
Best Local Similarity 98.4%; Pred. No. 3.3e-207;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;  
QY 1 MLLWVILLVAPVSGGFARTPRILFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60  
Db 1 MLLWVILLVAPVSGGFARTPRILFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60

QY 61 YLKGKILRETPDNILLEVQESGEYRCOAGSPSSPVHLDFSSASLILQAPLSVFEQDSV 120  
Db 61 YLKGKILRETPDNILLEVQESGEYRCOAGSPSSPVHLDFSSASLILQAPLSVFEQDSV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDPIPHACLKNDGAYRGTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDPIPHACLKNDGAYRGTGYKESCCPVSSNT 180  
QY 181 VKIQVQEPFTRPVLRASSPQISGNPVTLTCTQSLERSDVLPRFRDDQTILGLWS 240  
Db 181 VKIQVQEPFTRPVLRASSPQISGNPVTLTCTQSLERSDVLPRFRDDQTILGLWS 240  
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Db 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKALNPE 300  
QY 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
QY 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQSKAVSLIIVPVSHPVLTLSA 480  
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQSKAVSLIIVPVSHPVLTLSA 480  
QY 481 EALTPEGATVTLHCEVQSGSPQILLYQFYHEDMPLVSSSTPSVGRVSFSLSLTEGHSNGY 540  
Db 481 EALTPEGATVTLHCEVQSGSPQILLYQFYHEDMPLVSSSTPSVGRVSFSLSLTEGHSNGY 540  
QY 541 CTADNGFGPQSEVVSFLVTKCWVLASKPPL 572  
Db 541 CTADNGFGPQSEVVSFLVTKCWVLASKPPL 568

RESULT 5  
AAB82315  
ID AAB82315 standard; protein; 977 AA.  
XX AC AAB82315;  
XX DT 23-JUL-2001 (first entry)  
XX Human immunoglobulin receptor isoform IRTA2c.  
XX Immunoglobulin superfamily receptor translocation associated; IRTA;  
XX IRTA2c; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;  
XX myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Peptide 1..15  
XX Protein /label= Signal\_peptide  
XX Modified-site 16..977  
XX Modified-site 132..134  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 383..385  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 621..623  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 631..633  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 714..716  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 795..797  
XX Modified-site /note= "Asn is N-glycosylated"  
XX Modified-site 806..808  
XX Modified-site /note= "Asn is N-glycosylated"







Db 241 LSPNQITAMWSKDSGFYCKAAATMPHSHVSDSPRSWIOVQIPASHVPLTILSPKALNFE 300  
Qy 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360  
Db 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420  
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLITVPVSHVPLTILSSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLITVPVSHVPLTILSSA 480  
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540  
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540  
Qy 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 572  
Db 541 CTADNGFGPORSSEVSLFVT---VPVSRPIL 568

RESULT 8  
ABM82476  
ID ABM82476 standard; protein; 875 AA.  
XX AC ABM82476;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:2725.  
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX OS Homo sapiens.  
XX PN WO2004023973-A2.  
XX PD 25-MAR-2004.  
XX PF 12-SEP-2003; 2003WO-US028227.  
XX PR 12-SEP-2002; 2002US-0410259P.  
XX PR 12-SEP-2002; 2002US-0410260P.  
XX PA (INCY-) INCYTE CORP.  
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panear IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtzen ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX WPI: 2004-329368/30.  
XX DR N-PSDB; ACN41128.  
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX PS Claim 27; Page; 190pp; English.  
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX Sequence 875 AA;  
SQ Query Match 93.4%; Score 2918.5; DB 8; Length 875;  
Best Local Similarity 97.4%; Pred. No. 8.2e-205;  
Matches 557; Conservative 3; Mismatches 9; Indels 3; Gaps 1;  
Qy 1 MLLWVILLVLAAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTCKGRFRFSPQTKWYHR 60  
Db 1 MLLWVILLVLAAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTCKGRFRFSPQTKWYHR 60  
Qy 61 YLGKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFFSSASLILOAPLSVEGDSVV 120  
Db 61 YLGKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFFSSASLILOAPLSVEGDSVV 120  
Qy 121 LRCRKA AEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRKA AEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLWS 240  
Db 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLWS 240  
Qy 241 LSPNFOITAMWSKDSGFYCKAAATMPHSHVSDSPRSWIOVQIPASHVPLTILSPKALNFE 300  
Db 241 LSPNFOITAMWSKDSGFYCKAAATMPHSHVSDSPRSWIOVQIPASHVPLTILSPKALNFE 300  
Qy 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360  
Db 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420  
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLITVPVSHVPLTILSSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLITVPVSHVPLTILSSA 480  
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540  
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540  
Qy 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 572  
Db 541 CTADNGFGPORSSEVSLFVT---VPVSRPIL 569

RESULT 9  
ABM82477  
ID ABM82477 standard; protein; 837 AA.  
XX AC ABM82477;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:2726.  
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX OS Homo sapiens.  
XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV, Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH, Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patury S, Shi X, Suarez Cu;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN41129.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX SQ Sequence 837 AA;

Query Match 86.0%; Score 2685.5; DB 8; Length 837;

Best Local Similarity 90.6%; Pred. No. 9.1e-188;

Matches 518; Conservative 3; Mismatches 10; Indels 41; Gaps 2;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQKTWYHR 60

Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQKTWYHR 60

QY 61 YLGEKILRETPDNLVEQSGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFGDSVV 120

Db 61 YLGEKILRETPDNLVEQSGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFGDSVV 120

QY 121 LRCRAKAEVLNNTIYKNDVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180

Db 121 LRCRAKAEVLNNTIYKNDVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFQIPISGNPVLTICETQLSLERSDVPVLRFFRDQDTGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVLTICETQLSLERSDVPVLRFFRDQDTGLGWS 240

QY 241 LSPNFQITAMWSKDSGFGVCKAAATMPHSVLSDSRSMIQVQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFGVCKAAATMPHSVLSDSRSMIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360

Db 282 -----XFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 322

QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Db 323 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 382

QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTVPVSHPVLTLSA 480

Db 383 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTVPVSHPVLTLSA 442

QY 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540

Db 443 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 502

QY 541 CTADNGFGPORSVSVSLFVTGCKWVLASKPPL 572

Db 503 CTADNGFGPORSVSVSSFSLS---VPVSRPIL 531

RESULT 10

ABU99155

ID ABU99155 standard; protein; 582 AA.

XX AC ABU99155;

XX DT 01-AUG-2003 (first entry)

XX DE Novel human GPCR related protein NOV17a.

XX KW Human; G-protein coupled receptor related protein; GPCR related protein; NOV; cytostatic; cardiac; antiarteriosclerotic; antidiabetic; immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic; antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer; diabetes; immune disorder; AIDS; obesity; asthma; haematopoietic disorder; Parkinson's disease; Alzheimer's disease; infection; multiple sclerosis; cancer-associated cachexia; wasting disorder; chronic disease; neurogenesis; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

OS Homo sapiens.

XX WO200299116-A2.

XX PD 12-DEC-2002.

XX 04-JUN-2002; 2002WO-US017428.

XX 04-JUN-2001; 2001US-0295607P.

XX 04-JUN-2001; 2001US-0295661P.

XX 06-JUN-2001; 2001US-0296404P.

XX 06-JUN-2001; 2001US-0296418P.

XX 14-JUN-2001; 2001US-0298285P.

XX 15-JUN-2001; 2001US-0298556P.

XX 21-JUN-2001; 2001US-0299949P.

XX 26-JUN-2001; 2001US-0300883P.

XX 28-JUN-2001; 2001US-0301550P.

XX 13-AUG-2001; 2001US-0311972P.

XX 27-AUG-2001; 2001US-0315071P.

XX 29-AUG-2001; 2001US-0315660P.

XX 14-SEP-2001; 2001US-0322293P.

XX 17-SEP-2001; 2001US-0322706P.

XX 14-DEC-2001; 2001US-0341186P.

XX 28-FEB-2002; 2002US-0361189P.

XX 12-MAR-2002; 2002US-0363673P.

XX 03-JUN-2002; 2002US-0363676P.

(CURA-) CURAGEN CORP.

XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;

PI Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjal T, Kekuda R, Li L;  
PI MacDougall JR, Malvankar UM, Millet I, Padigaru M, Patturajan M;  
PI Pena CE, Rastelli L, Shimkets RA, Stone DU, Spytek KA, Vernet CAM;  
PI Voss EZ, Zerhusen BD;  
XX WPI: 2003-140627/13.  
DR N-PSDB; ACD03659.  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX Claim 1; Page 166; 332pp; English.  
XX The invention describes an isolated polypeptide (I) comprising any of 27  
CC 118-961 residue amino acid sequences, given in the specification, a  
CC mature form of them, a sequence that is at least 95 % identical to them,  
CC or a sequence having one or more conservative substitutions in them. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease selected from a pathology  
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides  
CC and antibodies are useful in treating or preventing NOVX-associated  
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
CC associated cachexia, and other wasting disorders associated with chronic  
CC diseases. The nucleic acids and polypeptides may also be used as targets  
CC for the identification of small molecules that modulate or inhibit e.g.  
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
CC wound healing and angiogenesis, in gene therapy, in generation of  
CC antibodies that bind immunospecifically to NOVX substances for use in  
CC therapeutic or diagnostic methods. The nucleic acids are further used as  
CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
CC medicine, and pharmacogenomics. The polypeptides are also useful as  
CC vaccines. This is the amino acid sequence of a novel human G-protein  
CC coupled receptor related protein NOV  
XX SQ Sequence 582 AA;  
Query Match 38.2%; Score 1193.5; DB 6; Length 582;  
Best Local Similarity 45.5%; Pred. No. 1.2e-78;  
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;  
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFGQVRLTCKGFRFYSPQ-KTKWYH 59  
DB 1 MLLWVILLVTPREGQGVAPKAVLLNPNPSTAFKGEKVALICSSISHSLAQDIWYH 60  
QY 60 RYLGKEILRTPDNILEVQSGEYRCQAQSGPLSPVHLDFSSASLILQAPLSVFGDSV 119  
DB 61 ---DEKLLTKHKDKI-QITEFGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFGDNV 116  
QY 120 VLRCAKAEVTLNNTIYKNDVLAFLNKRDFHIFACLKNDGAYRGTGYKESC---CPV 176  
DB 117 ILRCQKQKNDKNTQKVKYKDGKQLPNSYLEKIVTNSVRDNSKSYCHTAYRKFYLLDIEV 176  
QY 177 SSTNTKIQVQEPFTRPVLRASSFQPI-SGNPVTLTCTQLSLERSDPLRFRFRDDQTLG 236  
DB 177 TSFPLNIOVELFLHPLVLRASSFTPEGSPTWTLCTQLSPQDPVQLQSLFRDQTLG 236  
QY 237 LGWSLSPNFOITAMWSKDSGFYCKAATMPHSVISDSRSMIOVQ-IPASHPVLTLSPEK 295  
DB 237 LGWSRSPRLQIPAMWTEDSGYVCEVETVTHSIKGRSLRQIRVQRPVSVNVLNLEIRPTG 296  
QY 296 ALNFEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERGASISFSLTT---ENSGN 352  
DB 297 GQIEGENMVLICSAQSGSTVTFSSWHKEG-RVRSGLGRKTRQSLLAELHLVTLVKESDAGR 355  
QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHPLVNLSSPEDLIEFGAKVTLHCFAQSGSPILY 412  
DB 356 YYCAADNVHSPILSTWIRTVIRVPVSHPLVTFPRAPRAHTVVGDLLEHLCESLGRSPILY 415  
QY 413 QFHHDAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGQFQSRKAVSLSVTPVSH 472

Db 416 RFVHEDVTGNSAPSGGASFNLSLTAHSGNYSCDADNGLGAQHSHGVSRLRVTPVSR 475  
QY 473 PVLTSSAEALTPEGATVTLHCEVQVQSGPOILYQFYHEDMPLVSSSTPSPVGRVVSFSLT 532  
DB 476 PVLTTRAPGAQAVVGDLELHLCESLGRSPILYWFYHEDDTLGNISAHSGGASFNLSLT 535  
QY 533 EHGSGNYCTADNGFGQFQSRSEVVSFLVTG 561  
DB 536 TEHSGNYSCDADNGLGAQHSHGVSRLRVTPV 564  
RESULT 11  
ADM93875  
ID ADM93875 standard; protein; 582 AA.  
XX AC ADM93875;  
XX DT 17-JUN-2004 (first entry)  
XX DE Human NOV protein #47.  
XX KW gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;  
XX KW Parkinson's disease; metabolic disorder; diabetes; obesity;  
XX KW immune related disorder; tissue typing; human.  
XX OS Homo sapiens.  
XX PN US2004009480-A1.  
XX PD 15-JAN-2004.  
XX PF 03-JUN-2002; 2002US-00162335.  
XX PR 04-JUN-2001; 2001US-0295607P.  
XX PR 06-JUN-2001; 2001US-0295661P.  
XX PR 06-JUN-2001; 2001US-0296404P.  
XX PR 11-JUN-2001; 2001US-0296418P.  
XX PR 12-JUN-2001; 2001US-0297567P.  
XX PR 14-JUN-2001; 2001US-0298285P.  
XX PR 15-JUN-2001; 2001US-0298556P.  
XX PR 21-JUN-2001; 2001US-0299949P.  
XX PR 26-JUN-2001; 2001US-0300883P.  
XX PR 28-JUN-2001; 2001US-0301550P.  
XX PR 13-AUG-2001; 2001US-0311972P.  
XX PR 27-AUG-2001; 2001US-0315069P.  
XX PR 27-AUG-2001; 2001US-0315071P.  
XX PR 29-AUG-2001; 2001US-0315660P.  
XX PR 14-SEP-2001; 2001US-0322293P.  
XX PR 17-SEP-2001; 2001US-0322706P.  
XX PR 14-DEC-2001; 2001US-0341186P.  
XX PR 28-FEB-2002; 2002US-0361189P.  
XX PR 12-MAR-2002; 2002US-0363673P.  
XX PR 12-MAR-2002; 2002US-0363676P.  
XX (ANDE/) ANDERSON D W.  
PA (BAUM/) BAUMGARTNER J C.  
PA (BOLD/) BOLDG F L.  
PA (CASM/) CASMAN S J.  
PA (EDIN/) EDINGER S R.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUOX/) GUO X S.  
PA (HJAL/) HJALT T.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MALV/) MALVANKAR U M.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.

PA (PENA/) PENA C E A.  
PA (RST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
PA (STON/) STONE D J.  
PA (SPYT/) SPYTEK K A.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
XX  
XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;  
PI Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjalt T, Kekuda R, Li L;  
PI MacDougall JR, Malvankar UM, Millet I, Padigaru M, Patturajan M;  
PI Pena CE, Rastelli L, Shinkets RA, Stone DJ, Spytek KA, Vernet CM;  
PI Voss EZ, Zernhusen BD;  
XX  
XX WPI; 2004-090456/09.  
DR N-PSDB; ADM93874.  
XX  
XX New NOVX polypeptide, useful for preparing a composition for treating or  
PT preventing e.g., cancer, neurodegenerative disorders such as Parkinson's  
PT disease, or metabolic disorders such as diabetes or obesity, or for  
PT tissue typing.  
XX  
XX Claim 1; SEQ ID NO 94; 202pp; English.  
XX  
XX The invention relates to an isolated NOVX polypeptide. The polypeptide is  
CC useful for preparing a composition for treating or preventing a pathology  
CC associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders  
CC such as Parkinson's disease, metabolic disorders such as diabetes or  
CC obesity or immune related disorders or for tissue typing. The present  
CC sequence represents a human NOV protein.  
XX  
XX Sequence 582 AA;  
  
Query Match 38.2%; Score 1193.5; DB 8; Length 582;  
Best Local Similarity 45.5%; Pred. No. 1.2e-78;  
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;  
  
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRYSQ-KTKWH 59  
DB 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRYSQ-KTKWH 60  
  
QY 60 RYLKREILRETPDNLVEQSGEYRCQAGSPSSPVHLDFFSSASLILQAPLSVFEQDSV 119  
DB 61 ----DEKLLKHKDKI-QITEPGNYCKTGGSSLSDAVHVEFPDMLLQALHPVFGDNV 116  
  
QY 120 VLFRCRAAEVTLNNTIYKNDNLVAFLNKRTDFH PHACLKNGAYRCTGYKSC---CPV 176  
DB 117 ILRCQCKDNKNTHQVYKDGKQLPNSYNLEKITVNSVRDNSKVHCTAYRKFIYLDIEV 176  
  
QY 177 SNTVKIQVEPTFRVLEASSFQPIGPNPVLTCETQLSLERSDVPFLFRFRDDQTLG 236  
DB 177 TSXPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPDVLQFSLFRDSQTLG 236  
  
QY 237 LGWSLSPNFOITAMWKGDSFYKCKAATMPHSVISDPSRWIQV-IPASHVPLTILSPK 295  
DB 237 LGWSRSPRIQIPAMWEDSGSYCEVETVTHSIKSLRSQIEVQRPVSNVNLIRPTG 296  
  
QY 296 ALNFEGTKVTLHCETQEDSLRTLYRPHYHGVPLRHKSVCRCGASISFSLT---ENSGN 352  
DB 297 GQLIEGNMVLICSAVQSGSTVTFWSHKEG-RVRSGLRKTQRLSLLAEHLVLTIKESDAGR 355  
  
QY 353 YCTADNGLCAKSKAVSLSVTPVSHPLNLSSPEDLIFEGAKVTLHCBAQSGSPILY 412  
DB 356 YCAADNVHSPILSTVIRVTRIPVSHPLVTFRAPRAHTVVGDLLEHCELSRGSPPILY 415  
  
QY 413 QFHEDAALERRRANGAGGVAISFSITAEHSGNYCTADNGFGQSRKAVSLSIITPVSH 472  
DB 416 RFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSACDADNGLGAQSHGSLRVTPVSR 475  
  
QY 473 PVLTLASAEALTPEGATVTLHCEVQSGSPQILYQFHEDMPLVSSSTPVSGRVSFSLT 532  
DB 476 PVLTLAPGAQAVVGDLLEHCELSRGSFPILYFWFYHEDDTLGNISAHSGGGASFNLSLT 535

QY 533 EGHSGNYCTADNGFGQSRSEWSLFTVTG 561  
DB 536 TEHSGNYSCADNGLGAQSHKSVTLNVTG 564  
  
RESULT 12  
ADM06089  
ID ADM06089 standard; protein; 707 AA.  
XX  
AC ADM06089;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein of the invention SEQ ID NO:4774.  
XX  
KW human; gene therapy; diagnostic marker; pharmaceutical.  
XX  
OS Homo sapiens.  
XX  
FN EP1347046-A1.  
XX  
PD 24-SEP-2003.  
XX  
PF 12-APR-2002; 2002EP-00008400.  
XX  
PR 22-MAR-2002; 2002JP-00137785.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Izrie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX  
DR WPI; 2003-723558/69.  
DR N-PSDB; ADM03646.  
XX  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
PS Claim 1; SEQ ID NO 4774; 305pp; English.  
XX  
XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
SQ Sequence 707 AA;  
  
Query Match 38.2%; Score 1193.5; DB 7; Length 707;  
Best Local Similarity 45.5%; Pred. No. 1.5e-78;  
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;  
  
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRYSQ-KTKWH 59  
DB 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRYSQ-KTKWH 60  
  
QY 60 RYLKREILRETPDNLVEQSGEYRCQAGSPSSPVHLDFFSSASLILQAPLSVFEQDSV 119  
DB 61 ----DEKLLKHKDKI-QITEPGNYCKTGGSSLSDAVHVEFPDMLLQALHPVFGDNV 116  
  
QY 120 VLFRCRAAEVTLNNTIYKNDNLVAFLNKRTDFH PHACLKNGAYRCTGYKSC---CPV 176  
DB 117 ILRCQCKDNKNTHQVYKDGKQLPNSYNLEKITVNSVRDNSKVHCTAYRKFIYLDIEV 176  
  
QY 177 SNTVKIQVEPTFRVLEASSFQPIGPNPVLTCETQLSLERSDVPFLFRFRDDQTLG 236

```

Db 177 TSKPLNQVQLFHPVLRASSSTPIEGSPMTLTCETQLSPQRPDVQLQSLFRDSQTLG 236
Qy 237 LGWSLSNFQITAMWSKDSGFYWKCAATMPHSVSDSPRSMQIQV-IPASHPVLTLSPEK 295
Db 237 LGWSRSPKLIQIPAMWTEDSGSYMCVEVTVTHSIKKRSLRQIRVQRPVSNVNLIRPTG 296
Qy 296 ALNPEGTQVTLHCETQDSRLTYRFYHGVPLNKHVRCRGASISFSLTT---ENSGN 352
Db 297 GQLIEGNMVLICSVAGSGTTFVSMHKEG-RVRSGLRKTQRSLLAEHLVLTVKESDAGR 355
Qy 353 YYCTADNGLGAKPSKAVSLSVTVVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRTVTRIPVSHPVLTFRAPRAHTVVGDLLELHCSLRGSPILY 415
Qy 413 QFHEDAAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTTVPVSH 472
Db 416 RFYHEDVTILGNSSAPSGGASFNLSLTAHSGNYSCDADNGLGAQHSGLRVTVPVSR 475
Qy 473 PVLTLSSAEALTPEGATVTLHCEVQRGSPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLT 532
Db 476 PVLTLRAGAAVVGDLLELHCSLRGSPILYWFYHEDDTLGNISAHSGGASFNLSLT 535
Qy 533 EHGSGNYCTADNGFGPQRSVSLFVTG 561
Db 536 TEHSGNYSCEADNGLGAQHSKVTLNVTG 564

```

## RESULT 13

AA82316  
ID AAB82316 standard; protein; 734 AA.

XX AC AA82316;

XX DT 23-JUL-2001 (first entry)

XX DE Human immunoglobulin receptor IRTA3 protein.

XX KW Immunoglobulin superfamily receptor translocation associated; IRTA3;

XX KW human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;

XX KW B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

XX OS Homo sapiens.

XX PN WO200138490-A2.

XX PD 31-MAY-2001.

XX PF 28-NOV-2000; 2000WO-US032403.

XX PR 29-NOV-1999; 99US-0168151P.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Dalla-Favera R;

XX DR WPI; 2001-355921/37.

XX DR N-PSDB; AAF30953.

XX PT New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor  
Translocation Associated proteins, used to treat B cell malignancies  
including lymphomas and multiple myeloma.

XX PS Claim 4; Fig 18C-1-18C-2; 72pp; English.

XX CC The present sequence is that of the novel human immunoglobulin receptor,  
CC immunoglobulin superfamily receptor translocation associated protein 3  
CC (IRTA3), an Fc receptor involved in the pathogenesis of lymphoma and  
CC melanoma. Efforts to identify genes involved in chromosomal aberrations  
CC affecting band 1q21 in multiple myeloma and B cell lymphoma led to the  
CC discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a  
CC novel subfamily of related receptors within the immunoreceptor family. 3  
CC Additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were

CC subsequently identified, which are also members of this novel subfamily.  
CC The IRTA genes display a specific pattern of expression in mature B  
CC cells. IRTA3 is expressed in GC centrocytes and in perifollicular cells,  
CC which may include lymphoblasts and memory cells. This is analogous to  
CC IRTA2 expression. The invention provides IRTA nucleic acids and proteins,  
CC and antibodies directed to an epitope of an IRTA protein. Methods are  
CC claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal  
CC rearrangement using a nucleic acid molecule that specifically hybridises  
CC with a unique sequence of human IRTA1-5; and treating a subject having a  
CC B cell cancer by administering an anti-IRTA antibody or an antisense  
CC oligonucleotide that specifically hybridises to IRTA mRNA so as to  
CC prevent overexpression of IRTA protein and hence to arrest cell growth or  
CC induce cell death of cancer cells expressing IRTA. The B cell cancer is  
CC selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma,  
CC Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma,  
CC and follicular lymphoma. The B cell lymphoma is selected from mucosa-  
CC associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma  
XX  
XX Sequence 734 AA;

Query Match 38.2%; Score 1193.5; DB 4; Length 734;  
Best Local Similarity 45.5%; Pred. No. 1.6e-78;  
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

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Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPTVTVFOGERVTLCKGRFRFYSPQ-KTKWYH 59
Db 1 MLLWLLLLILTPGREQSGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQDITYYH 60
Qy 60 RYLKKEILRETPDNILEVOESGEYRCQAQGSPLSSPVHLDFSSASLTQLAPLSVFEGDSV 119
Db 61 ---DEKLLIKIKDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLTLQALHPVFGDNV 116
Qy 120 VLRCKRAEVTNLNTIYKNDNLVLAFLNKRDFHPIHACKLNDGAYRCTGYKESC---CPV 176
Db 117 ILRCQCKDNKTHQKYKDGKQLPNSYNLEKTVNSVSRDNSKYHCTARKFYLDIEV 176
Qy 177 SSNTVKIQVQEPFTRPVLRASSFPQISGNPVTUTCTQLSLERSDVLPRFRFRDDQTLG 236
Db 177 TSKPLNIQVQLFHPVLRASSSTPIEGSPMTLTCETQLSPQRPDVQLQSLFRDSQTLG 236
Qy 237 LGWSLSNFQITAMWSKDSGFYWKCAATMPHSVSDSPRSMQIQV-IPASHPVLTLSPEK 295
Db 237 LGWSRSPKLIQIPAMWTEDSGSYMCVEVTVTHSIKKRSLRQIRVQRPVSNVNLIRPTG 296
Qy 296 ALNPEGTQVTLHCETQDSRLTYRFYHGVPLNKHVRCRGASISFSLTT---ENSGN 352
Db 297 GQLIEGNMVLICSVAGSGTTFVSMHKEG-RVRSGLRKTQRSLLAEHLVLTVKESDAGR 355
Qy 353 YYCTADNGLGAKPSKAVSLSVTVVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRTVTRIPVSHPVLTFRAPRAHTVVGDLLELHCSLRGSPILY 415
Qy 413 QFHEDAAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTTVPVSH 472
Db 416 RFYHEDVTILGNSSAPSGGASFNLSLTAHSGNYSCDADNGLGAQHSGLRVTVPVSR 475
Qy 473 PVLTLSSAEALTPEGATVTLHCEVQRGSPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLT 532
Db 476 PVLTLRAGAAVVGDLLELHCSLRGSPILYWFYHEDDTLGNISAHSGGASFNLSLT 535
Qy 533 EHGSGNYCTADNGFGPQRSVSLFVTG 561
Db 536 TEHSGNYSCEADNGLGAQHSKVTLNVTG 564

```

## RESULT 14

ADM35238

ID ADM35238 standard; protein; 734 AA.

XX AC ADM35238;

XX DT 03-JUN-2004 (first entry)



DE Human LY1448P cancer related protein for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;  
KW chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

XX 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample  
PT from the patient with a binding agent that binds to a cancer-associated  
PT polypeptide and comparing the amount of polypeptide to a predetermined  
PT cutoff value.

XX Disclosure; SEQ ID NO 10463; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient  
CC by: (i) contacting a biological sample from the patient with an agent  
CC that binds to any of three polypeptides given in the specification; (ii)  
CC detecting in a sample an amount of the peptide that binds to the binding  
CC agent; and (iii) comparing the amount of polypeptide present in the  
CC patient's sample to a predetermined cutoff value. The specification also  
CC discloses a separate method for detecting (M2) cancer in a patient by a  
CC method similar to M1, except that the detection agent is an  
CC oligonucleotide that binds to any of three polynucleotides given in the  
CC specification. M1 and M2 are useful for detecting the presence of cancer  
CC in a patient, especially chronic lymphocytic leukemia. The applicants  
CC have identified specific human polypeptides overexpressed in one or more  
CC types of hematological malignancies. This sequence corresponds to a  
CC protein used in the method of the invention.

XX Sequence 734 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 734;

Best Local Similarity 45.5%; Pred. No. 1.6e-78;

Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWILLVLAVPSGQFARTPRPIIFLOPPWTTVFGERVTLTCKGFRFYSPO-KTKVWH 59

DB 1 MLLWILLVLITGRQSGVAPKAVALLNPNWSTAFKGEKVALICSIHSLAQGTYVWH 60

QY 60 RYLKGEILRETPDNILEVOESGEYRCQAGSPFLSPVHLDFSSALILQAPLSVFEGBSV 119

DB 61 ---DEKLLIKHKDKI-QITEPGNYCKTRGSSLSDAVHVFPSPDMLILQALHPVEGDV 116

QY 120 VLRCRAKEVTLNNTIKYNDVLAFLNKRTDHPHACLKONGAYRCCTGYKESC---CPV 176

DB 117 ILRCQKGNKNTHQKYVYKQGLPNSNLEKITVNSVSRDMSKYHTAYRKFYILDIEV 176

QY 177 SSNTVKIQVQEPFTRPVLRASSFPQISGNPVTCTQLSLERSVPLRFRFRDDQTLG 236

DB 177 TSKPNIQVQELFLHPVLRASSSTIEGSPMTLTCTQLSPQPDVQVQSLFRSQTLG 236

QY 237 LGWSLSPNQITAMWSKDSGFYCKAAATMPHSVIDSPRSWTQVQ-IPASHVPLTISPEK 295

DB 237 LGWSRSPRLQIPAMWTEDSGSVCEVETVTHSIKKRSLRSQIRVQRPVSNVNLIRPTG 296

QY 296 ALNFGTKVTLHCETQEDSLRLTYFYHGVPLRHKSVRCERGASISLSLT---ENSGN 352

DB 297 GOLIEGNMVLICSAQSGTGTTFGSMHKEG-RVRSIGRKTQRSLLAELHLVLTVESDAGR 355

QY 353 YYCTADNGLGAKPSKAVSLSVTPVSPVSHVNLSSPEDLIFEGAKVTLHCEAQSGSLPILY 412

DB 356 YYCAADNVHSPILSTWIRVTPVSPVSHVNLSSPEDLIFEGAKVTLHCEAQSGSLPILY 415

QY 413 QPHHEDAAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLISITVPVSH 472

DB 416 RPYHEDVTLGNSSAPSGGASFNLSLTAHSGNYSCTADNGLGQAQSHGVSLRVTPVSR 475

QY 473 PVLTLSSAALTFEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLIT 532

DB 476 PVLTLRAPGAQAVVGDLLHLCESLRGSPFPLYFYHEDDTLGNISAHSGGASFNLSIT 535

QY 533 EGHSGNYYCTADNGFGPQSGPQSEVWSLFTVG 561

DB 536 TEHSGNYSCEADNGLGQAQSHGVSLRVTLNVG 564

RESULT 15

ABM84916

ID ABM84916 standard; protein; 750 AA.

XX AC ABM84916;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5165.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN43568.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithio protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 750 AA;

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Query Match      38.2%; Score 1193.5; DB 8; Length 750;
Best Local Similarity 45.5%; Pred. No. 1.7e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

Qy 1 MLLWVILLVLAPSGQFARTPRPIIFLPQWTVTFQGERVTLCKGRFRFYSPQ-KIKWYH 59
Db 1 MLLWVILLVLAPSGQFARTPRPIIFLPQWTVTFQGERVTLCKGRFRFYSPQ-KIKWYH 59
Qy 60 RYLKGEILRETPDNILVQESGEYRCAQSGPLSPVHLDFFSSASLILQAPLSVFEGDSV 119
Db 61 ---DEKLUKIKHDKI-QITEFGNYQCKIRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRKTDHFHAPHACLKDNAGYRCTGYKESC--CPV 176
Db 117 ILRCQKDNKNTKQVYKQKQLPNSYNLEKITVNSVRDNSKYCHTAIRKFVILDIEV 176
Qy 177 SSNTVKIQVQEPFTRPVLRASSPOISGNPVTLTCETQLSLERSDVLPRFRFRDDQTLG 236
Db 177 TSKPLNTIQVQELFLHPVLRASSPTIEGSPMTLTCTQLSPQRPDVQLQPSLFRDSQTLG 236
Qy 237 LGWSLSNFOITAMWSKDSGFYCKAATMPHSVTSDSFRSMIQVO-IPASHPVLTLSPEX 295
Db 237 LGWSRSRPLQIPAMWTEDSGSYCEVETVTHSIKKRSLRQIRVQRPVPSNVNLEIRPTG 296
Qy 296 ALNPEGKVTILHCETQSDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTT---ENSGN 352
Db 297 GQLIEGENWVLI CSVAGSGTVTFSEWKEG-RVPSLGRKTRQSLLAELHVLITVKESDAGR 355
Qy 353 YYCTADNGLGAKPSKAVSLVTVVPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRVTIRIPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSPPILY 415
Qy 413 QPHHEDAALERSNSAGGVAISFSLTAHSGNYCTADNGFGPQORSKAVSLITVPSH 472
Db 416 RFYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYSCDADNGLGAQSHGSLRVTVEVSR 475
Qy 473 PVLTLSSAEALTPEGAVTTLHCEVQSGPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLT 532
Db 476 PVLTLRAPGAQVVGDLLELHCESLRGSPFILLWFYHEDDTLGNISAHSGGGASFNLSLT 535
Qy 533 EHGSGNYCTADNGFGPQSEVSLFVTG 561
Db 536 TEHSGNYSCADNGLGAQHSKVTLNVTG 564
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Search completed: May 4, 2005, 11:32:40  
Job time : 80.2887 secs





361	QY	LGAKPSKAVLSVTVPVSHPVNLSSPEDLIFEKAVTLHCEAQRGSLPILYQFHEDAA	420
836	DB	LGAKPSKAVLSVTVPVSHPVNLSSPEDLIFEKAVTLHCEAQRGSLPILYQFHEDAA	895
421	QY	LERRANSAGGVAIFSILTAHSGNYICTADNGFPORSKAVLSITVPVSHPVLTLSA	480
896	DB	LERRANSAGGVAIFSILTAHSGNYICTADNGFPORSKAVLSITVPVSHPVLTLSA	955
481	QY	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHCNYY	540
956	DB	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHCNYY	1015
541	QY	CTADNGFPORSVWSLFTVTKCWVLASKPPLAE	574
1016	DB	CTADNGFPORSVWSLFTVTSRPLILTVRPQAQ	1049

RESULT 3  
US-09-245-764-7  
; Sequence 7, Application US/09245764  
; Patent No. 6675105  
; GENERAL INFORMATION:  
; APPLICANT: Hogarth, P. Mark  
; APPLICANT: Powell, Maree S.  
; APPLICANT: McKenzie, Ian F.C.  
; APPLICANT: Maxwell, Kelly F.  
; APPLICANT: Garrett, Thomas P.J.  
; APPLICANT: Epa, Vidana  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS  
; FILE REFERENCE: 4102-4  
; CURRENT APPLICATION NUMBER: US/09/245, 764  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: 60/099, 994  
; EARLIER FILING DATE: 1998-09-11  
; EARLIER APPLICATION NUMBER: 60/073, 972  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-245-764-7

Query Match	12.4%;	Score 386;	DB 4;	Length 261;
Best local Similarity	35.7%;	Pred. No. 6.7e-27;		
Matches	95;	Conservative	40;	Mismatches 121; Indels 10; Gaps 6
QY	20	TPRPILFLOPPTVTFQGSERVTLCKGRFYSPKTKWVHYRLGKEILRETPD--NILE	76	
DB	1	TTKAVITLQPPVSVFQEBETVTLCEVHLPGSSSTQMFVN--GTATOTSTPSYRITSAS	58	
QY	77	VQSGSVRCQAQGSPLSPGVHLDFSASLIIQLAPLSVF--EGDSVVLRCRAAEVTLNNTI	135	
DB	59	VNDSGEYRCQRLSGSDPIQLEIHRGWLLQLQVSSRVFTEGEPLARCCHAWKDKLYNYVL	118	
QY	136	YKQNDNLVAFUNKRDTPHIACLKNGAYRCTGYKSCCPVSNTVKVIOCEPFTFPLVR	195	
DB	119	YVRNGKFKFPHMNSNITLKTINISNGTYHCSGMGKH--RYSAGISVTVVKELFPAPVLN	176	
QY	196	ASSFQP--ISGNPVTLTCETQLSLERSDVPLFRFRFRDDQTLGLGWSLSPNFQITAMWSD	254	
DB	177	ASVTSPLLEGVNLVTLSCETKLLKQRPGLQLVFSFYMGSKTL--RGRNTSSSYQLTARRD	235	
QY	255	SGFYWCKAAATMPSHVISDSRPSWIOV	280	
DB	236	SGLYWCEAAATEDGNVLKRSPELQV	261	

RESULT 4  
US-08-667-939A-3  
; Sequence 3, Application US/08667939A

776	QY	776	GTKVTLHCEQDSRLTLRFYHEGVPLRHKSVRCERGASISFSLSTTENSQNYCTADNG	835
361	QY	361	LGAQPSKAVLSVTVPVSHPVNLNSPEDLIIEGAKVTLHCEAQRGSLPILYQPHHDEAA	420
836	Db	836	LGAQPSKAVLSVTVPVSHPVNLNSPEDLIIEGAKVTLHCEAQRGSLPILYQPHHDEAA	895
421	QY	421	LERRANSAGGVAISFSLTAEHSGNYCTADNGFGQPSKAVLSITVPVSHVLTLSA	480
896	Db	896	LERRANSAGGVAISFSLTAEHSGNYCTADNGFGQPSKAVLSITVPVSHVLTLSA	955
481	QY	481	EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPVSGRVSFSLTEGHSQNY	540
956	Db	956	EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPVSGRVSFSLTEGHSQNY	1015
541	QY	541	CTADNGFGQPSQSEVVSFLVTGKCWLAKPEPLAE	574
1016	Db	1016	CTADNGFGQPSQSEVVSFLVTGSRPILTLRVFRAQ	1049

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RESULT 2
US-09-949-016-10596
; Sequence 10596, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10596
; LENGTH: 1248
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10596

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Query Match	94.5%;	Score 2953;	DB 4;	Length 1248;
Best local Similarity	97.9%;	Pred. No. 7, 8e-260;		
Matches 562;	Conservative	3;	Mismatches	9;
			Indels	0;
			Gaps	0;
Qy	1	MLLWVILLVAPVSGGFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR	60	
Db	476	MLLWVILLVAPVSGGFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR	535	
Qy	61	YLGEIILRETPDNILEVQESGEYRCQAQSPVHLDFDSASLILQAPLSVEGDSVV	120	
Db	536	YLGEIILRETPDNILEVQESGEYRCQAQSPVHLDFDSASLILQAPLSVEGDSVV	595	
Qy	121	LRCRAKAEVTLNNTIYKDNVLAFLNKRITDFHIFACLKDNQAYRCTGYKSSCCPVSNT	180	
Db	596	LRCRAKAEVTLNNTIYKDNVLAFLNKRITDFHIFACLKDNQAYRCTGYKSSCCPVSNT	655	
Qy	181	VKIQVQEPFTRPVLRASSFQIPSGNPVLTCTEQSLERSDVPILRFRFRDDQTLGLWS	240	
Db	656	VKIQVQEPFTRPVLRASSFQIPSGNPVLTCTEQSLERSDVPILRFRFRDDQTLGLWS	715	
Qy	241	LSPNFOITAMWSKDSGGYWCKAATMPSHVISDSPRSWIOVQIPASHPVLTLSPEKALNFE	300	
Db	716	LSPNFOITAMWSKDSGGYWCKAATMPSHVISDSPRSWIOVQIPASHPVLTLSPEKALNFE	775	
Qy	301	GTKVTLHCETOEDSILRTLYRPHYEGVPLRHKSVRCRGASISFSLTTSNGNYYCTADNG	360	
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RESULT 5
US-06433-123-3
? Sequence 3, Application US/08433123
? Patent NO. 644789
? GENERAL INFORMATION:
? APPLICANT: LUO, Shun
? TITLE OF INVENTION: CD16-II VARIANTS
? NUMBER OF SEQUENCES: 25
? CORRESPONDENCE ADDRESS:
?

```

Thu May 5 15:10:58 2005

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/667,939A  
FILING DATE: 24-JUN-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/433,123  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LUO=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-667-939A-2

Query Match 9.7%; Score 304.5; DB 2; Length 254;  
Best Local Similarity 32.9%; Pred. No. 1.7e-19;  
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;  
QY 1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58  
Db 4 LLLPTALLLVASGMRTEPLKAVVLEPQWYVLEKDSVTLKCOG--AYSPEDNSTQWF 61  
QY 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQSPSSPVHLDFFSSASLI 106  
Db 62 HK-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEVQVGWLL 110  
QY 107 LOAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHPIHACLKNGAY 164  
Db 111 LOARWVFKEDPIHLRCHSWKNTALHKVTYLONGKDRKYFHNSDFHPIKATLKDSGY 170  
QY 165 RCTGKSCCVPSSNTVKIQVQEFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPL 224  
Db 171 FCKGLVGS-KNVSETVNTIIOGLA--VSTNSSFFP-PGYQVSF-CLVMVLLFAVD-- 223  
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261  
Db 224 -----GLYFSVKTNRSTSRDWDKHKFKWK 249

RESULT 7  
US-08-433-123-2  
Sequence 2, Application US/08433123  
Patent No. 6444789  
GENERAL INFORMATION:  
APPLICANT: LUO, Shun  
TITLE OF INVENTION: CD16-II VARIANTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/433,123

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LUO=2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-433-123-2

Query Match 9.7%; Score 304.5; DB 4; Length 254;  
Best Local Similarity 32.9%; Pred. No. 1.7e-19;  
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;  
QY 1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58  
Db 4 LLLPTALLLVASGMRTEPLKAVVLEPQWYVLEKDSVTLKCOG--AYSPEDNSTQWF 61  
QY 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQSPSSPVHLDFFSSASLI 106  
Db 62 HK-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEVQVGWLL 110  
QY 107 LOAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHPIHACLKNGAY 164  
Db 111 LOARWVFKEDPIHLRCHSWKNTALHKVTYLONGKDRKYFHNSDFHPIKATLKDSGY 170  
QY 165 RCTGKSCCVPSSNTVKIQVQEFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPL 224  
Db 171 FCKGLVGS-KNVSETVNTIIOGLA--VSTNSSFFP-PGYQVSF-CLVMVLLFAVD-- 223  
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261  
Db 224 -----GLYFSVKTNRSTSRDWDKHKFKWK 249

RESULT 8  
US-10-006-011A-2  
Sequence 2, Application US/10006011A  
Patent No. 6821947  
GENERAL INFORMATION:  
APPLICANT: Iozzo, Renato V.  
TITLE OF INVENTION: Endorepellin: methods and compositions  
TITLE OF INVENTION: for inhibiting angiogenesis  
FILE REFERENCE: 8321-95  
CURRENT APPLICATION NUMBER: US/10/006,011A  
CURRENT FILING DATE: 2001-12-04  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 4391  
TYPE: PRT  
ORGANISM: human  
US-10-006-011A-2

Query Match 9.6%; Score 299.5; DB 4; Length 4391;  
Best Local Similarity 23.5%; Pred. No. 4e-17;  
Matches 145; Conservative 90; Mismatches 264; Indels 117; Gaps 28;  
QY 23 PIIFLOPPWTVFQGERVTLTKGFRFYSQK-TKWYHYLGKELRETPDNIL-----E 76  
Db 2630 PPRIESSPTVEGQTLDCVVAR--QPAITWYKGGSLPSRHOTGSHLHOMS 2687  
QY 77 VQSSGEYRCQAQ-----GSP-----LSSPVHLDFFSSASLIQAPLSVF 114



Db 2688 VADSGEYVCRANNIDALEASIVISVPSAGSPAGSSMEIRIESSSS-----HVA 2739  
Qy 115 EGDSVLRCRAKAEVTLNNTIYKNDNVLA--FLNKRDTDFHHPHACLKNDGAYRC-----T 167  
Db 2740 EGETDLNLCVVPQAHAQVTHKRGSLPSHHQTRGSRRLRHVSPADSGEYVCRVMGSS 2799  
Qy 168 GYKESCCPV-----SNTVKIQVEBPTFRVLRL--ASSFQIPISGNPVTLC-----ETQLS 216  
Db 2800 GPLEASLVLTIEASGSAVHPAPCGAPPRIEFPSSGRVAREGQTLDLKCVVPGQAHAQVT 2859  
Qy 217 LER--SDVPLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWK-----AATMPSHV- 269  
Db 2860 WHKGGNLPARHGVH-----GPLLRLNQVSPADSGEYSCQVTGSSGTLEASVL 2907  
Qy 270 ISDSPRWMIQVQIPASHPVLTLSPEKALNPEGTKVTLHCETQEDSLRTLRFYHEG--VP 327  
Db 2908 VTIEPSPGPPIAPGLAQPIYIEASSSHVTGQTLNLCVVPQA--HAQVTVYKRGGSLLP 2966  
Qy 328 LRKHSVRCERGASISFSLTT--ENSGNYCYCTADNGLGAKPKANVLSLTVTPVSH----- 379  
Db 2967 ARHQT-----HGSQLRLHLVSPADSGEYVCRASGPG--PEQEAFTVTVPPSEGSYRLR 3020  
Qy 380 -PVNLSSPEDLIEGAKVTLHCEAQRGSLPILYQEHHEDAALERRRANSAGGVAISFSL 438  
Db 3021 SPVLSIDPPSTVOQQDASFCLIHDAAPISLEWTRNQELEDNWHISPNGSIITVIG 3080  
Qy 439 T-AEHSNGNYCTADNFGPQPSKAVLSITVPVSHPVLTLSABALTFEGATVTLHCEVQ 497  
Db 3081 TRPSNHGTYRCVASNAYGAQS--VNLVSHGPPT--VSVLPEGPVWVKVKAIVLEC-VS 3136  
Qy 498 RGSPOILYQFHEMDPLVSPSTPSGRVSRFSFSLTEGH-----SGNYCYCTADN 545  
Db 3137 AGEPRSSARWTR-----ISSTPA-KLEQRTYGLMDSHAVLIQISAKPSPDAGTYVCLAQN 3189  
Qy 546 GFGPQRSEVWSLFTVG 561  
Db 3190 ALGTAQKQVEVIVDTG 3205

RESULT 9  
US-08-667-939A-6  
; Sequence 6, Application US/08667939A  
; Patent No. 5998166  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,939A  
; FILING DATE: 24-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/433,123  
; FILING DATE: 03-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:

Db 2688 VADSGEYVCRANNIDALEASIVISVPSAGSPAGSSMEIRIESSSS-----HVA 2739  
Qy 115 EGDSVLRCRAKAEVTLNNTIYKNDNVLA--FLNKRDTDFHHPHACLKNDGAYRC-----T 167  
Db 2740 EGETDLNLCVVPQAHAQVTHKRGSLPSHHQTRGSRRLRHVSPADSGEYVCRVMGSS 2799  
Qy 168 GYKESCCPV-----SNTVKIQVEBPTFRVLRL--ASSFQIPISGNPVTLC-----ETQLS 216  
Db 2800 GPLEASLVLTIEASGSAVHPAPCGAPPRIEFPSSGRVAREGQTLDLKCVVPGQAHAQVT 2859  
Qy 217 LER--SDVPLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWK-----AATMPSHV- 269  
Db 2860 WHKGGNLPARHGVH-----GPLLRLNQVSPADSGEYSCQVTGSSGTLEASVL 2907  
Qy 270 ISDSPRWMIQVQIPASHPVLTLSPEKALNPEGTKVTLHCETQEDSLRTLRFYHEG--VP 327  
Db 2908 VTIEPSPGPPIAPGLAQPIYIEASSSHVTGQTLNLCVVPQA--HAQVTVYKRGGSLLP 2966  
Qy 328 LRKHSVRCERGASISFSLTT--ENSGNYCYCTADNGLGAKPKANVLSLTVTPVSH----- 379  
Db 2967 ARHQT-----HGSQLRLHLVSPADSGEYVCRASGPG--PEQEAFTVTVPPSEGSYRLR 3020  
Qy 380 -PVNLSSPEDLIEGAKVTLHCEAQRGSLPILYQEHHEDAALERRRANSAGGVAISFSL 438  
Db 3021 SPVLSIDPPSTVOQQDASFCLIHDAAPISLEWTRNQELEDNWHISPNGSIITVIG 3080  
Qy 439 T-AEHSNGNYCTADNFGPQPSKAVLSITVPVSHPVLTLSABALTFEGATVTLHCEVQ 497  
Db 3081 TRPSNHGTYRCVASNAYGAQS--VNLVSHGPPT--VSVLPEGPVWVKVKAIVLEC-VS 3136  
Qy 498 RGSPOILYQFHEMDPLVSPSTPSGRVSRFSFSLTEGH-----SGNYCYCTADN 545  
Db 3137 AGEPRSSARWTR-----ISSTPA-KLEQRTYGLMDSHAVLIQISAKPSPDAGTYVCLAQN 3189  
Qy 546 GFGPQRSEVWSLFTVG 561  
Db 3190 ALGTAQKQVEVIVDTG 3205

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-667-939A-6

Query Match 9.4%; Score 293; DB 2; Length 233;  
Best Local Similarity 34.7%; Pred. No. 1.7e-18;  
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

Qy 1 MLLMVLIVLAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVLSAGMRTEDLPKAVFLEPQWRYRLEKDSVTLKCGQ--AYSPEDNSTQWF 61  
Qy 59 HRYLGKILRETPDNILE-----VOESGEYRCQAQGSPLSPVHLDSSASLI 106  
Db 62 HN-----ENLISSQASSYFIDAATVDDSGEYRCQNLSTLSDPVQLEHVHVGWLL 110  
Qy 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHHPHACLKNDGAY 164  
Db 111 LQAPRWVFKBEDPIHLRCHSKWKTALHKVTVYLONGKDRKYFHNSDFHHPKATLKDSGY 170  
Qy 165 RCTGYKESCCPVSNVTVKIQVEBPTFRVLRLRASSFPQISGNPVTLCETQLSLERSDVL 224  
Db 171 FCRGLVGS-KNVSSSETVNTITOGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDVTGL 225  
Qy 225 RF 226  
Db 226 YF 227

RESULT 10  
US-08-433-123-6  
; Sequence 6, Application US/08433123  
; Patent No. 6444789  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,123  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-433-123-6

Query Match 9.4%; Score 293; DB 4; Length 233;  
Best Local Similarity 34.7%; Pred. No. 1.7e-18;  
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPO--KTKWY 58  
DB 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61  
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSSPVHLDFFSSASLI 106  
DB 62 HN-----ENLSSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHGLL 110  
QY 107 LQAPLSVF-EGSVVLRCAKAEVTLNNTIY-KDNVLAFLNKRDFHPIHACLKNGAY 164  
DB 111 LQAPRWVFEEDPIHLRCHSWKNTALHKVTVLQNGKDRKYFHNSDFPIPKATLKDSGS 170  
QY 165 RCTGYKESCCPVSSNTVKIQVEPFRPVLRRASSFPISGNPVTITCETQLSLERSD 224  
DB 171 FCRGLVGS-KVNSSETVNTITQGLA--VSTISSFP-PGYQVSP-CLVMVLLFAVD 225  
QY 225 RF 226  
DB 226 YF 227

RESULT 11  
US-08-667-939A-9  
; Sequence 9, Application US/08667939A  
; Patent No. 5938166  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,939A  
; FILING DATE: 24-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/433,123  
; FILING DATE: 03-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2A  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-667-939A-9

Query Match 9.4%; Score 292.5; DB 2; Length 254;  
Best Local Similarity 33.1%; Pred. No. 2.1e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

QY 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPO--KTKWY 58

DB 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61  
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSSPVHLDFFSSASLI 114  
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHGLLQAPRWV 118  
QY 115 -EGSVVLRCAKAEVTLNNTIY-KDNVLAFLNKRDFHPIHACLKNGAYRCTGYKES 172  
DB 119 KEEPIHLRCHSWKNTALHKVTVLQNGKDRKYFHNSDFPIPKATLKDSGSYFCRGLFGS 178  
QY 173 CCPVSSNTVKIQVEPFRPVLRRASSFPISGNPVTITCETQLSLERSDVP 232  
DB 179 -KVNSSETVNTITQGLA--VSTISSFP-PGYQVSP-CLVMVLLFAVD 223  
QY 233 QTLGLWSLSNFQITAMWSKDSGFYWK 261  
DB 224 ---GLYFSVKTNIIRSTRDMKDKFKWRK 249

RESULT 12  
US-08-433-123-9  
; Sequence 9, Application US/08433123  
; Patent No. 6444789  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,123  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-433-123-9

Query Match 9.4%; Score 292.5; DB 4; Length 254;  
Best Local Similarity 33.1%; Pred. No. 2.1e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

QY 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPO--KTKWY 58  
DB 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61  
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSSPVHLDFFSSASLI 114  
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHGLLQAPRWV 118

QY 115 -EGDSVVLRCRAKAEVTNNIY-KNDNLVAFLNKRTDHPHACLKNGAYRCTGYKES 172  
 Db 119 KEEDPIHLRCHSWKNTALHKVYTLQNGKRGKRYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
 QY 173 CCPVSSNTVKIQOEPFTRPVLRASSFPQISGNPVTLTCTETQLSLERSDVLPRFRFRDD 232  
 Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227  
 QY 233 QTLGLWSLSPNFOITAMWKSOGFYWCK 261  
 Db 224 ---GLFSVKTNRSTRSDWKDKFKWRK 249

RESULT 13  
 US-08-667-939A-5  
 ; Sequence 5, Application US/08667939A  
 ; Patent No. 5998166  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LUO, Shun  
 ; TITLE OF INVENTION: CD16-II VARIANTS  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/667,939A  
 ; FILING DATE: 24-JUN-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/433,123  
 ; FILING DATE: 03-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: LUO-2A  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 233 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-667-939A-5

Query Match 9.3%; Score 292; DB 2; Length 233;  
 Best Local Similarity 35.5%; Pred. No. 2.1e-18;  
 Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPPTVTFQGERVTLTKGFRFYSPQ--KTKWY 58  
 Db 4 LLLPTALLLVASGMRTEPLKAVVFLPQWYVLEKSDVTLKCG--AYSPEDNSTQWF 61  
 QY 59 HRYLGEILRETPDNL---EVOESGEYRCQAGSPVHLDPFSSASLILOAPLSVF 114  
 Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQVLEHVHIGWLLQAPRWVF 118  
 QY 115 -EGDSVVLRCRAKAEVTNNIY-KNDNLVAFLNKRTDHPHACLKNGAYRCTGYKES 172  
 Db 119 KEEDPIHLRCHSWKNTALHKVYTLQNGKRGKRYFHNSDFYIPKATLKDSGSYFCRGLVGS 178  
 QY 173 CCPVSSNTVKIQOEPFTRPVLRASSFPQISGNPVTLTCTETQLSLERSDVLPRF 226  
 Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227

RESULT 15  
 US-08-433-123-5  
 ; Sequence 5, Application US/08433123  
 ; Patent No. 6444789  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LUO, Shun  
 ; TITLE OF INVENTION: CD16-II VARIANTS

Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227

RESULT 14  
 US-08-667-939A-8  
 ; Sequence 8, Application US/08667939A  
 ; Patent No. 5998166  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LUO, Shun  
 ; TITLE OF INVENTION: CD16-II VARIANTS  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/667,939A  
 ; FILING DATE: 24-JUN-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/433,123  
 ; FILING DATE: 03-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: LUO-2A  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 233 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-667-939A-8

Query Match 9.3%; Score 292; DB 2; Length 233;  
 Best Local Similarity 35.5%; Pred. No. 2.1e-18;  
 Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

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 Db 4 LLLPTALLLVASGMRTEPLKAVVFLPQWYVLEKSDVTLKCG--AYSPEDNSTQWF 61  
 QY 59 HRYLGEILRETPDNL---EVOESGEYRCQAGSPVHLDPFSSASLILOAPLSVF 114  
 Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQVLEHVHIGWLLQAPRWVF 118  
 QY 115 -EGDSVVLRCRAKAEVTNNIY-KNDNLVAFLNKRTDHPHACLKNGAYRCTGYKES 172  
 Db 119 KEEDPIHLRCHSWKNTALHKVYTLQNGKRGKRYFHNSDFYIPKATLKDSGSYFCRGLVGS 178  
 QY 173 CCPVSSNTVKIQOEPFTRPVLRASSFPQISGNPVTLTCTETQLSLERSDVLPRF 226  
 Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227

RESULT 15  
 US-08-433-123-5  
 ; Sequence 5, Application US/08433123  
 ; Patent No. 6444789  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LUO, Shun  
 ; TITLE OF INVENTION: CD16-II VARIANTS

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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUGO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-5

Query Match          9.3%; Score 292; DB 4; Length 233;
Best Local Similarity 35.5%; Pred. No. 2.1e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVLLVLPVSGQFARTPRPIIFLQPPWTVFGERVVTITCKGFRFYSPQ--KTKWY 58
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 4 LLLPTALLLVLSAGMRTDLPKAVVLEPQWYVLEKSDVTLKCGQ--AYSPEDNSTQWF 61
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 59 HRYLKGKELRTPDNIL----EYQESGEYECQAGSPLSSPVHLDFSSASLILOAPLSVF 114
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 62 H---NESLISSQASSYFIDAATVNDSGEYRCQNLSTLSDPVQLEVGHGWLQLQAPRWVF 118
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 115 -EGDSWVLCRAKAEVTLNNITY--KNDNVLAFLNKTDFPHIACLKONGAYRCTGYKES 172
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 119 KEEDPIHLRCHSWKNNTALHKVYTLQNGKDKRYFHNSDFPHI KATLKDSGSYFCRGLVGS 178
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 173 CCFVSGNTVKIQVQEPFTRPVLVRASSQPTISGNPVTILTCETQLSLERSVPLRF 226
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Db 179 -KNVSSSEVTNITITQGLA--VSTISYSSFSF-PGYQVSP-CLVMVLLPFAVDITGLYF 227
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Job time : 20.8351 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 62.811 Seconds  
(without alignments)  
3139.559 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence: 1 MLLMWILLVLAVPSGQFART.....AEFSLTHSFKNLFAISFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3111	99.6	592	14	US-10-040-862-10461 Sequence 10461, A
2	3111	99.6	592	15	US-10-057-475B-10461 Sequence 10461, A
3	3111	99.6	592	15	US-10-154-884B-10461 Sequence 10461, A
4	3111	99.6	592	15	US-10-403-847-8 Sequence 8, Appli
5	3111	99.6	592	16	US-10-764-324-10461 Sequence 10461, A
6	2950	94.4	759	14	US-10-040-862-10460 Sequence 10460, A
7	2950	94.4	759	15	US-10-057-475B-10460 Sequence 10460, A
8	2950	94.4	759	15	US-10-154-884B-10460 Sequence 10460, A
9	2950	94.4	759	15	US-10-403-847-7 Sequence 7, Appli
10	2950	94.4	759	16	US-10-764-324-10460 Sequence 10460, A
11	2950	94.4	977	14	US-10-040-862-10462 Sequence 10462, A
12	2950	94.4	977	14	US-10-241-220-97 Sequence 97, Appl
13	2950	94.4	977	15	US-10-057-475B-10462 Sequence 10462, A

14	2950	94.4	977	15	US-10-154-884B-10462 Sequence 10462, A
15	2950	94.4	977	15	US-10-403-847-9 Sequence 9, Appli
16	2950	94.4	977	16	US-10-764-324-10462 Sequence 10462, A
17	2924.5	93.6	790	15	US-10-403-847-4 Sequence 4, Appli
18	1854	59.3	438	15	US-10-403-847-6 Sequence 6, Appli
19	1502	48.1	317	15	US-10-403-847-2 Sequence 2, Appli
20	1193.5	38.2	582	15	US-10-162-335-94 Sequence 94, Appl
21	1193.5	38.2	707	15	US-10-108-260A-4774 Sequence 4774, Ap
22	1193.5	38.2	734	14	US-10-040-862-10463 Sequence 10463, A
23	1193.5	38.2	734	15	US-10-057-475B-10463 Sequence 10463, A
24	1193.5	38.2	734	15	US-10-154-884B-10463 Sequence 10463, A
25	1193.5	38.2	734	16	US-10-764-324-10463 Sequence 10463, A
26	1193.5	38.2	734	17	US-10-948-518-137 Sequence 137, App
27	1176	37.6	727	17	US-10-473-519-20 Sequence 20, Appl
28	900	28.8	181	16	US-10-363-829-286 Sequence 286, App
29	900	28.8	181	16	US-10-363-829-431 Sequence 431, App
30	847.5	27.1	639	16	US-10-408-765A-2410 Sequence 2410, Ap
31	826.5	26.5	515	14	US-10-040-862-10459 Sequence 10459, A
32	826.5	26.5	515	15	US-10-057-475B-10459 Sequence 10459, A
33	826.5	26.5	515	15	US-10-154-884B-10459 Sequence 10459, A
34	826.5	26.5	515	16	US-10-764-324-10459 Sequence 10459, A
35	803.5	25.7	421	15	US-10-162-335-96 Sequence 96, Appl
36	803.5	25.7	421	15	US-10-162-335-98 Sequence 98, Appl
37	791	25.3	152	15	US-10-403-847-10 Sequence 10, Appl
38	786.5	25.2	421	15	US-10-162-335-100 Sequence 100, App
39	783.5	25.1	445	15	US-10-154-884B-11043 Sequence 11043, A
40	773.5	24.8	508	14	US-10-040-862-10464 Sequence 10464, A
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43	773.5	24.8	508	15	US-10-154-884B-11039 Sequence 11039, A
44	773.5	24.8	508	16	US-10-764-324-10464 Sequence 10464, A
45	773.5	24.8	508	17	US-10-948-518-119 Sequence 119, App

ALIGNMENTS

RESULT 1

- US-10-040-862-10461
- Sequence 10461, Application US/10040862
- Publication No. US20030078396A1
- GENERAL INFORMATION:
- APPLICANT: Gaiger, Alexander
- APPLICANT: Algate, Paul A.
- APPLICANT: Mannion, Jane
- APPLICANT: Retter, Marc
- APPLICANT: Corixa Corporation
- TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of Hematological Malignancies
- FILE REFERENCE: 014058-013520US
- CURRENT APPLICATION NUMBER: US/10/040,862
- CURRENT FILING DATE: 2001-11-06
- PRIOR APPLICATION NUMBER: US 60/186,126
- PRIOR FILING DATE: 2000-03-01
- PRIOR APPLICATION NUMBER: US 60/190,479
- PRIOR FILING DATE: 2000-03-17
- PRIOR APPLICATION NUMBER: US 60/200,545
- PRIOR FILING DATE: 2000-04-27
- PRIOR APPLICATION NUMBER: US 60/200,303
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,779
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,999
- PRIOR FILING DATE: 2000-05-01
- PRIOR APPLICATION NUMBER: US 60/202,084
- PRIOR FILING DATE: 2000-05-04
- PRIOR APPLICATION NUMBER: US 60/206,201
- PRIOR FILING DATE: 2000-05-22
- PRIOR APPLICATION NUMBER: US 60/218,950
- PRIOR FILING DATE: 2000-07-14
- PRIOR APPLICATION NUMBER: US 60/222,903
- PRIOR FILING DATE: 2000-08-03
- PRIOR APPLICATION NUMBER: US 60/223,416

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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10461

Query Match          99.6%; Score 3111; DB 14; Length 592;
Best Local Similarity 99.7%; Pred. No. 5.8e-235;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
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Db 61 YLGKEILRETPDNILEVQESGEGYRCQAQSPVHLDFFSSASLILQAPLSVFEGDSV 120
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Db 121 LRCRAKAEVTNNTIYKNDNVLAFLNKRTDFH PHACLKDNAGYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPTFRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRPRDDQDTLGLWS 240
Db 181 VKIQVEPTFRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRPRDDQDTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNPE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNPE 300
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QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSTVPSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSTVPSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
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Db 541 CTADNGFGPQRSEVSLFTGKWCWLASKPPPLAEFSLTHSFKNLFALSFLP 592
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## RESULT 2

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US-10-057-475B-10461
; Sequence 10461, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
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; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10461
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Query Match          99.6%; Score 3111; DB 15; Length 592;
Best Local Similarity 99.7%; Pred. No. 5.8e-235;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
QY 61 YLGKEILRETPDNILEVQESGEGYRCQAQSPVHLDFFSSASLILQAPLSVFEGDSV 120
Db 61 YLGKEILRETPDNILEVQESGEGYRCQAQSPVHLDFFSSASLILQAPLSVFEGDSV 120
QY 121 LRCRAKAEVTNNTIYKNDNVLAFLNKRTDFH PHACLKDNAGYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTNNTIYKNDNVLAFLNKRTDFH PHACLKDNAGYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPTFRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRPRDDQDTLGLWS 240
Db 181 VKIQVEPTFRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRPRDDQDTLGLWS 240
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RESULT 3  
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; Sequence 10461, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154, 884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10461  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-154-884B-10461

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Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQERVTLTKGFRFYSPQTKWYHR 60

Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120  
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLWS 240  
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLWS 240

Qy 241 LSNPFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300  
Db 241 LSNPFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLIPLYQPHHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLIPLYQPHHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQORSKAVSLSIITVPVSHPVLTLSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQORSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540  
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540

Qy 541 CTADNGFQORSEVSVLFTGKCVLASKPPLABFSLTHSPKNI.FALSSFLP 592  
Db 541 CTADNGFQORSEVSVLFTGKCVLASHPPLABFSLTHSPKNI.FALSSFLP 592

RESULT 4  
US-10-403-847-8  
; Sequence 8, Application US/10403847  
; Publication No. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403, 847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368, 671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371, 420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-847-8

Query Match 99.6%; Score 3111; DB 15; Length 592;  
Best Local Similarity 99.7%; Pred. No. 5.8e-235;  
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQERVTLTKGFRFYSPQTKWYHR 60  
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQERVTLTKGFRFYSPQTKWYHR 60

Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120  
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLWS 240  
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLWS 240

Qy 241 LSNPFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300  
Db 241 LSNPFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLIPLYQPHHEDAA 420



Db

361

LGAKPSKAVSLSVTVVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPIYLQFHEDAA

420

Qy

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Db

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Qy

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Db

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Qy

541

CTADNGFGPQRSEVSVLFTVGKWCWLASKPPLAEFSLTHSPKMLFALSFLP

592

Db

541

CTADNGFGPQRSEVSVLFTVGKWCWLASHPPPLAEFSLTHSPKMLFALSFLP

592

RESULT 5

US-10-764-324-10461

/ Sequence 10461, Application US/10764324

/ Publication No. US20040175739A1

/ GENERAL INFORMATION:

/ APPLICANT: Gaiger, Alexander

/ APPLICANT: Algate, Paul A.

/ APPLICANT: Mannion, Jane

/ APPLICANT: Retter, Marc

/ APPLICANT: Corixa Corporation

/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

/ TITLE OF INVENTION: Hematological Malignancies

/ FILE REFERENCE: 014058-013520US

/ CURRENT APPLICATION NUMBER: US/10/764,324

/ CURRENT FILING DATE: 2004-01-23

/ PRIOR APPLICATION NUMBER: US/10/040,862

/ PRIOR FILING DATE: 2001-11-06

/ PRIOR APPLICATION NUMBER: US 60/186,126

/ PRIOR FILING DATE: 2000-03-01

/ PRIOR APPLICATION NUMBER: US 60/190,479

/ PRIOR FILING DATE: 2000-04-27

/ PRIOR APPLICATION NUMBER: US 60/200,303

/ PRIOR FILING DATE: 2000-04-28

/ PRIOR APPLICATION NUMBER: US 60/200,779

/ PRIOR FILING DATE: 2000-04-28

/ PRIOR APPLICATION NUMBER: US 60/200,999

/ PRIOR FILING DATE: 2000-05-01

/ PRIOR APPLICATION NUMBER: US 60/202,084

/ PRIOR FILING DATE: 2000-05-04

/ PRIOR APPLICATION NUMBER: US 60/200,545

/ PRIOR FILING DATE: 2000-05-04

/ PRIOR APPLICATION NUMBER: US 60/206,201

/ PRIOR FILING DATE: 2000-05-22

/ PRIOR APPLICATION NUMBER: US 60/218,950

/ PRIOR FILING DATE: 2000-07-14

/ PRIOR APPLICATION NUMBER: US 60/222,903

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: US 60/223,416

/ PRIOR FILING DATE: 2000-08-04

/ PRIOR APPLICATION NUMBER: US 60/223,378

/ PRIOR FILING DATE: 2000-08-07

/ PRIOR APPLICATION NUMBER: US 09/796,692

/ PRIOR FILING DATE: 2001-03-01

Db

361

LGAKPSKAVSLSVTVVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPIYLQFHEDAA

420

Qy

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Db

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Qy

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Db

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Qy

541

CTADNGFGPQRSEVSVLFTVGKWCWLASKPPLAEFSLTHSPKMLFALSFLP

592

Db

541

CTADNGFGPQRSEVSVLFTVGKWCWLASHPPPLAEFSLTHSPKMLFALSFLP

592

RESULT 6

US-10-040-862-10460

/ Sequence 10460, Application US/10040862

/ Publication No. US20030078396A1

/ GENERAL INFORMATION:

/ APPLICANT: Gaiger, Alexander

/ APPLICANT: Algate, Paul A.

/ APPLICANT: Mannion, Jane

/ APPLICANT: Retter, Marc

/ APPLICANT: Corixa Corporation

/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

/ TITLE OF INVENTION: Hematological Malignancies

/ FILE REFERENCE: 014058-013520US

/ CURRENT APPLICATION NUMBER: US/10/040,862

/ CURRENT FILING DATE: 2001-11-06

/ PRIOR APPLICATION NUMBER: US 60/186,126

/ PRIOR FILING DATE: 2000-03-01

/ PRIOR APPLICATION NUMBER: US 60/190,479

/ PRIOR FILING DATE: 2000-03-17

/ PRIOR APPLICATION NUMBER: US 60/200,545

/ PRIOR FILING DATE: 2000-04-27

/ PRIOR APPLICATION NUMBER: US 60/200,303

/ PRIOR FILING DATE: 2000-04-28

/ PRIOR APPLICATION NUMBER: US 60/200,779

/ PRIOR FILING DATE: 2000-04-28

/ PRIOR APPLICATION NUMBER: US 60/200,999

/ PRIOR FILING DATE: 2000-05-01

/ PRIOR APPLICATION NUMBER: US 60/202,084

/ PRIOR FILING DATE: 2000-05-04

/ PRIOR APPLICATION NUMBER: US 60/200,545

/ PRIOR FILING DATE: 2000-05-04

/ PRIOR APPLICATION NUMBER: US 60/206,201

/ PRIOR FILING DATE: 2000-05-22

/ PRIOR APPLICATION NUMBER: US 60/218,950

/ PRIOR FILING DATE: 2000-07-14

/ PRIOR APPLICATION NUMBER: US 60/222,903

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: US 60/223,416

/ PRIOR FILING DATE: 2000-08-04

/ PRIOR APPLICATION NUMBER: US 60/223,378

/ PRIOR FILING DATE: 2000-08-07

/ PRIOR APPLICATION NUMBER: US 09/796,692

/ PRIOR FILING DATE: 2001-03-01

Db

361

LGAKPSKAVSLSVTVVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPIYLQFHEDAA

420

Qy

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Db

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Qy

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Db

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Qy

541

CTADNGFGPQRSEVSVLFTVGKWCWLASKPPLAEFSLTHSPKMLFALSFLP

592

Db

541

CTADNGFGPQRSEVSVLFTVGKWCWLASHPPPLAEFSLTHSPKMLFALSFLP

592

Query Match

Best Local Similarity

Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Score 3111; DB 16; Length 592;

Pred. No. 5.8e-235;

1 MLLWVLLVLPVSGQFARTPRPIIFLOPWTWVFGQSVTLTKGFRFYSPOKTKWYHR

60

1 MLLWVLLVLPVSGQFARTPRPIIFLOPWTWVFGQSVTLTKGFRFYSPOKTKWYHR

60

61 YLGEILRETPDNLVEQESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQGSVV

120

61 YLGEILRETPDNLVEQESGEYRCQAGSPVHLDFSSASLILQAPLSVFEQGSVV

120

121 LRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT

180

Db

121

LRCRAKAEVTLNNTIYKNDNLVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT

180

Qy

181

VKIQVQPPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLRRFRFRDDOTLGLWS

240

Db

181

VKIQVQPPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLRRFRFRDDOTLGLWS

240

Qy

241

LSPNFQITAMWSKDSGYWCKAATMHSVILSDSPRMIQVQIPASHPVLTLSPEKALNFE

300

Db

241

LSPNFQITAMWSKDSGYWCKAATMHSVILSDSPRMIQVQIPASHPVLTLSPEKALNFE

300

Qy

301

GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCRGASISFSLTTENSNGNYCTADNG

360

Db

301

GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCRGASISFSLTTENSNGNYCTADNG

360

Qy

361

LGAKPSKAVSLSVTVVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPIYLQFHEDAA

420

Db

361

LGAKPSKAVSLSVTVVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPIYLQFHEDAA

420

Qy

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Db

421

LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVSHVPLTLSSA

480

Qy

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Db

481

EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSPFSFSLTEGHSNYY

540

Qy

541

CTADNGFGPQRSEVSVLFTVGKWCWLASKPPLAEFSLTHSPKMLFALSFLP

592

Db

541

CTADNGFGPQRSEVSVLFTVGKWCWLASHPPPLAEFSLTHSPKMLFALSFLP

592

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; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match          94.4%; Score 2950; DB 14; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60

Qy 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120
Db 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHIHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHIHACLKONGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480

Qy 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTECHSGNYY 540
Db 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTECHSGNYY 540

Qy 541 CTADNGFGPQRSEVSVSLFVTGKWCWLAKSKPPL 572
Db 541 CTADNGFGPQRSEVSVSLFVTGKWCWLAKSKPPL 572

RESULT 7
US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10460

Query Match          94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60

Qy 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120
Db 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHIHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHIHACLKONGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480

Qy 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTECHSGNYY 540
Db 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTECHSGNYY 540

Qy 541 CTADNGFGPQRSEVSVSLFVTGKWCWLAKSKPPL 572
Db 541 CTADNGFGPQRSEVSVSLFVTGKWCWLAKSKPPL 572
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## RESULT 8

US-10-154-884B-10460  
; Sequence 10460, Application US/10154884B.  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154, 884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10460  
; LENGTH: 759  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-154-884B-10460

Query Match 94.4%; Score 2950; DB 15; Length 759;  
Best Local Similarity 98.4%; Pred. No. 3.3e-22;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYHR	60
DB	1	MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYHR	60
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVY	120
DB	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVY	120
QY	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHI PHACLKDNAGYRCTGYKESCCPVSSNT	180
DB	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHI PHACLKDNAGYRCTGYKESCCPVSSNT	180
QY	181	VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVLPRFRFRDDQDTLGLWS	240
DB	181	VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVLPRFRFRDDQDTLGLWS	240
QY	241	LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
DB	241	LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG	360
DB	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA	420

DB	361	LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA	480
DB	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA	480
QY	481	EALTFEAGATVTLHCEVORGSPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY	540
DB	481	EALTFEAGATVTLHCEVORGSPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY	540
QY	541	CTADNGFGPQRSEVVSFLVTKCWVLASKPPL	572
DB	541	CTADNGFGPQRSEVVSFLVTKCWVLASKPPL	572

## RESULT 9

US-10-403-847-7  
; Sequence 7, Application US/10403847  
; Publication No. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICING VARIANTS OF A HUMAN  
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BOS5G AND BOS51  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403,847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371,420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 759  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-847-7

Query Match 94.4%; Score 2950; DB 15; Length 759;  
Best Local Similarity 98.4%; Pred. No. 3.3e-22;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYHR	60
DB	1	MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYHR	60
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVY	120
DB	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVY	120
QY	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHI PHACLKDNAGYRCTGYKESCCPVSSNT	180
DB	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHI PHACLKDNAGYRCTGYKESCCPVSSNT	180
QY	181	VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVLPRFRFRDDQDTLGLWS	240
DB	181	VKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSDVLPRFRFRDDQDTLGLWS	240
QY	241	LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
DB	241	LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG	360
DB	301	GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA	420
DB	361	LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA	480

```
Db 421 LERRSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
Db 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
Qy 541 CTADNGFGPORSSEVSVSLFVTGKCVLASKPPL 572
Db 541 CTADNGFGPORSSEVSVSLFVT----VPVSRPIL 568

RESULT 10
US-10-764-324-10460
; Sequence 10460, Application US/10764324
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 94.4%; Score 2950; DB 16; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPQTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPQTKWYHR 60
Qy 61 YLGEILRETPDNLVEQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQGSVV 120
Db 61 YLGEILRETPDNLVEQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQGSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQPIGNSPNVTLCETOLSLERSDVPVLRFRFRDDQTLGLGWS 240
```

```
Db 181 VKIQVQEPFTRPVLRASSFQPIGNSPNVTLCETOLSLERSDVPVLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCXKAATMPHSVSDSPRSMIQVOIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCXKAATMPHSVSDSPRSMIQVOIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVLSVTVPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVLSVTVPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVLSITVPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
Db 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
Qy 541 CTADNGFGPORSSEVSVSLFVTGKCVLASKPPL 572
Db 541 CTADNGFGPORSSEVSVSLFVT----VPVSRPIL 568

RESULT 11
US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
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Query Match 94.4%; Score 2950; DB 14; Length 977;  
Best Local Similarity 98.4%; Pred. No. 4.7e-222;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

1 MLLWVILLVAPVSGGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQKTKWYHR 60  
1 MLLWVILLVAPVSGGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQKTKWYHR 60

61 YLKEITLRETPDNILEVOESGEYRCAQSPVHLDFSSASLILQAPLSVFEGLSVV 120  
61 YLKEITLRETPDNILEVOESGEYRCAQSPVHLDFSSASLILQAPLSVFEGLSVV 120

121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180  
121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180

181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240  
181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240

241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPKALNFE 300  
241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPKALNFE 300

301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360  
301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360

361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIIFEGAKVTLHCEAORGSLPILYQFHEDAA 420  
361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIIFEGAKVTLHCEAORGSLPILYQFHEDAA 420

421 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480  
421 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540  
481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540

541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 572  
541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 572

541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 568  
541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 568

RESULT 13  
US-10-057-475B-10462  
; Sequence 10462, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clappet, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779

Query Match 94.4%; Score 2950; DB 14; Length 977;  
Best Local Similarity 98.4%; Pred. No. 4.7e-222;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

1 MLLWVILLVAPVSGGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQKTKWYHR 60  
1 MLLWVILLVAPVSGGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQKTKWYHR 60

61 YLKEITLRETPDNILEVOESGEYRCAQSPVHLDFSSASLILQAPLSVFEGLSVV 120  
61 YLKEITLRETPDNILEVOESGEYRCAQSPVHLDFSSASLILQAPLSVFEGLSVV 120

121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180  
121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180

181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240  
181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240

241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPKALNFE 300  
241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPKALNFE 300

301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360  
301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360

361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIIFEGAKVTLHCEAORGSLPILYQFHEDAA 420  
361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIIFEGAKVTLHCEAORGSLPILYQFHEDAA 420

421 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480  
421 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540  
481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540

541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 572  
541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 572

541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 568  
541 CTADNGFGPQRSSEVSVLFTCKWVLSKPPIL 568

RESULT 12  
US-10-241-220-97  
; Sequence 97, Application US/10241220  
; Publication No. US20030148408A1  
; GENERAL INFORMATION:  
; APPLICANT: Frantz, Gretchen  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Phillips, Heidi  
; APPLICANT: Polakis, Paul  
; APPLICANT: Spencer, Susan  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wu, Thomas  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5010R1-US  
; CURRENT APPLICATION NUMBER: US/10/241,220  
; CURRENT FILING DATE: 2002-12-13  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 97  
; LENGTH: 977  
; TYPE: PR1  
; ORGANISM: Homo Sapien  
US-10-241-220-97

; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-057-475B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPOKTKWYHR 60
QY 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVPEGDSVV 120
DB 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSQFISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSQFISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTFSGVRSFSLTEGHSNYY 540
DB 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTFSGVRSFSLTEGHSNYY 540
QY 541 CTADNGFGPORSEVWSLFTVTKGCWVLASKPPL 572
DB 541 CTADNGFGPORSEVWSLFTVTKGCWVLASKPPL 572

RESULT 14

US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-884B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPOKTKWYHR 60
QY 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVPEGDSVV 120
DB 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSQFISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSQFISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTFSGVRSFSLTEGHSNYY 540

Db 541 CTADNGFGPQRSEVSLFVT----VPVSRPIL 568

Search completed: May 4, 2005, 12:01:15  
Job time : 64.811 secs

Db 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540  
QY 541 CTADNGFGPQRSEVSLFVTGKCWLASKPPL 572  
Db 541 CTADNGFGPQRSEVSLFVT----VPVSRPIL 568

RESULT 15  
US-10-403-847-9  
; Sequence 9, Application US/10403847  
; Publication NO. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN  
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGS5G AND BGS5I  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403,847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR FILING DATE: U.S. 60/368,671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371,420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 977  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-847-9

Query Match 94.4%; Score 2950; DB 15; Length 977;  
Best Local Similarity 98.4%; Pred. No. 4.7e-222;  
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;  
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTVFQGERVTLTCKGFRFYSQKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTVFQGERVTLTCKGFRFYSQKTKWYHR 60  
QY 61 YLKGKILRETPDNIIEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSVY 120  
Db 61 YLKGKILRETPDNIIEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSVY 120  
QY 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTFHPHACLKNDGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTFHPHACLKNDGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVQPPFTRPVLRASSFPISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
Db 181 VKIQVQPPFTRPVLRASSFPISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSHIQVQIPASHPVLTLSPKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSHIQVQIPASHPVLTLSPKALNFE 300  
QY 301 GTKVTLCETQEDSLRTLRYREYHGVPLRHKSVCERGAISFSLTTENSGNYCTADNG 360  
Db 301 GTKVTLCETQEDSLRTLRYREYHGVPLRHKSVCERGAISFSLTTENSGNYCTADNG 360  
QY 361 LGAKPSKAVLSVTPVPSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420  
Db 361 LGAKPSKAVLSVTPVPSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSSA 480  
QY 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540  
Db 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540  
QY 541 CTADNGFGPQRSEVSLFVTGKCWLASKPPL 572



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:24:30 ; Search time 18.5636 Seconds  
(without alignments)  
3068.392 Million cell updates/sec

Title: US-09-724-254A-3  
Perfect score: 3124  
Sequence: 1 MLLWVILLVLPVSGQFART.....AEPSLTHSFKNLPSLSFLP 592

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418.5	13.4	344	2 A41357	Fc gamma (IgG) rec
2	418.5	13.4	374	1 A39878	Fc gamma (IgG) rec
3	402.5	12.9	404	2 A46480	Fc gamma (IgG) rec
4	396	12.7	336	2 I48471	Fc gamma (IgG) rec
5	326.5	10.5	296	2 I46021	Fc-gamma receptor
6	319	10.2	270	2 A34636	Fc-gamma receptor
7	299.5	9.6	4391	2 A38096	perlecan precursor
8	292.5	9.4	254	1 JL0107	Fc gamma (IgG) rec
9	292	9.3	233	1 JU0284	Fc gamma (IgG) rec
10	290	9.3	323	2 S06946	Fc gamma (IgG) rec
11	289	9.3	310	2 JL0119	Fc gamma (IgG) rec
12	275	8.8	7962	2 I38436	SH2 domain-contain
13	272	8.7	255	2 JC7593	elastic titin - hu
14	267	8.5	257	2 S00682	IgE Fc receptor al
15	264.5	8.5	317	2 JL0118	Fc gamma (IgG) rec
16	262	8.4	285	2 S36903	Fc gamma (IgG) rec
17	258	8.3	3707	2 S18252	heparan sulfate pr
18	257	8.2	261	2 S29360	Fc gamma (IgG) rec
19	256	8.2	280	2 I55577	Fc gamma (IgG) rec
20	253.5	8.1	283	1 FCMG31	Fc gamma (IgG) rec
21	253.5	8.1	330	2 A40071	Fc gamma (IgG) rec
22	253.5	8.1	330	2 I49660	Fc-gamma-1/gamma-2
23	248.5	8.0	1256	2 T03096	CDO protein - rat
24	248.5	8.0	738	2 A40096	platelet-endotheli
25	244	7.8	267	2 I56110	Fc-gamma RIIB- $\alpha$ p
26	241	7.7	1694	2 S00655	sialoadhesin - mou
27	241	7.7	1896	2 T08851	Down syndrome cell
28	240	7.7	862	2 I49583	differentiation an
29	235.5	7.5	1240	2 T03097	CDO protein - huma

ALIGNMENTS

RESULT 1

A41357

Fc gamma (IgG) receptor I (high affinity) form b - human

N;Alternate names: CD64

C;Species: Homo sapiens (man)

C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004

C;Accession: A41357; S03019

R;Allen, J.M.; Seed, B.

Science 243, 378-381, 1989

A;Title: Isolation and expression of functional high-affinity Fc receptor complementary I

A;Reference number: A41357; MUID:89100284; PMID:2911749

A;Accession: A41357

A;Molecule type: mRNA

A;Residues: 1-344 <ALL1>

A;Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; PID:G31334

R;Allen, J.M.; Seed, B.

Nucleic Acids Res. 16, 11824, 1988

A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR

A;Reference number: S03018; MUID:89098339; PMID:2974947

A;Accession: S03019

A;Molecule type: mRNA

A;Residues: 1-344 <ALL2>

A;Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334

A;Note: the authors translated the codon ACT for residue 25 as Ala

C;Superfamily: Fc gamma receptor I; immunoglobulin homology

C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein

F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 13.4%; Score 418.5; DB 2; Length 344;

Best Local Similarity 37.0%; Pred. No. 8.2e-21;

Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGRFRFVSPKTKVYHR 60

Db 7 LLLWV-----PVDGG-VDTTKAVITLOPPWVSVFQETVTLRCEVHLHLPSSSTOMFLN 59

Qy 61 YLGKEILRETPD---NILEVQESGEYRCAQGSPLSSPVHLDFFSSASLILOAPLSVF-EG 116

Db 60 --GTATQTSTPSYRITSASVNDGSEYRCQGLSGRSDPTQLEIHRGWLLQVSRVFTG 117

Qy 117 DSVLRCRA-KAEVLTNTIYKNDNVLAFLNKRKTDPHIACILKNDGAYRCTGYKESCCP 175

Db 118 EPLALACHAWKDKLVNVLVYRNGKAFKFFHWSNLTILKTNISHGTYHSCGMGKH--R 175

Qy 176 VSSNTVKIQVEPFTFPVLRASSFPQ-ISGNPVTLCETQLSLERSDVPLRFFRRDQT 234

Db 176 YTSAGISVTVKELFPAPVLNASVTSLELGNLVTLSCTKLLQRPGLQLYFYSFGSKT 235

Qy 235 LGIGWLSLNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOV---QIP 283

Db 236 L-RGRNTSEYQILTARRSDSLGYWCEAATDGNVLKRSPELEQLVLGLQLP 286

CD22 homolog/B lym  
carcinoembryonic a  
BIG-1 protein - ra  
Fc gamma (IgG) rec  
B-cell adhesion pr  
immunoglobulin-lik  
axonal glycoprotei  
IgE receptor alpha  
connectin 3B - chi  
connectin/titin -  
axonin 1 precursor  
hypothetical prote  
hemictentin precurs  
cell adhesion prot  
hypothetical prote  
plasmacytoma-assoc

```

Db      60  --GTATQTSTPSYRITSASVNDSEYRCQGLSGRSDPIQLIHRGMLLLQVSSRVFTG 117
117    DSVVLRCA-KAEVTLNNTIYKNDVLAFLNKRDTDFHAPHACLKNDGAYRCTGYKESCCP 175
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
118    EPLALRCHAWKDKLVVNVLYRNGKAFKFFHWNLSLTLKTNISNGYHCSGMGKH--R 175
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
176    VSNNTVKIQVQPFTRPVLRASSFOF-ISGNPVTTLTCTQLSLERSDVLPRFRFRDQOT 234
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
176    YTSAGISVTKKELFAPVNLNASVTSPLLEGLVTLSCETKLLQRPGLQYFSFYNGSKT 235
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235    LGLGWSLSNPFQITAMWSKDSGFYCKWKAATMPSHVISDSPRSWIQV--QIP 283
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236    L-RGRNTSSEYQILTARREDSGLYWCAAATDGNVLRKSPLELQVLGLQLP 286
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
A6480
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IGG receptor
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Cross-references: UNIPROT:P26151
A>Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NCI
R:Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for Igg
A:Reference number: A43511; MUID:90111035; PMID:2136886
A:Accession: A43511
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <SEA>
A:Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
C:127-179/Domain: immunoglobulin homology <IM>

Query Match 12.9%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 1.2e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY      3    LWVI--LLVLAPVSGQFARTPRPIFLQPPWTVTFQGERVTLTKGFRFYSPQTKWYHR 60
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10    MWLLTLLLVPEVGVVNAVTKAVITLQPPWVSIFQKENVTLWCEGPHLPDGSSTQWFIN 69
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      61    YLQKEILRETPDNIL---EVOESGEYRCQAQSPGLSSPVHLDFFSSASILQAPLSVVF-EG 116
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      70    --GTAVQISTPSYSIPEASFDQSGEYRCQIGSSMPSDPVLQIHNDWLLQASRVLTG 127
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      117    DSVVLRCA-KAEVTLNNTIYKNDVLAFLNKRDTDFHAPHACLKNDGAYRCTGYKESCCP 175
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      128    EPLALRCHGWKDKLVVNVLYRNGKSFQF-SSDSEVALKTNLSHGSIYHCSGTRH--R 184
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      176    VSNNTVKIQVQPFTRPVLRASSFOPI-SGNPVTTLTCTQLSLERSDVLPRFRFRDQOT 234
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      185    YTSAGISVTKKELFTTPVLRASVSSFPFPGSLVTLNCTNLLQLQRPGLQYFSFYNGSKI 244
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      235    LGLGWSLSNPFQITAMWSKDSGFYCKWKAATMPSHVISDSPRSWIQVQIP-ASHPV 288
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      245    LEYR-NTSSEYHIAAREDAGYWCVEVATDSSVLKRSPELELQVLGLQYFSFYNGSKI 298
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
148471
Fc gamma (IgG) receptor high affinity - mouse

```

C/Species: Mus musculus (house mouse)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C/Accession: I48471  
R/Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff  
Science 260, 695-698, 1993  
A>Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for IgG  
A/Reference number: I48471; MUID:93242399; PMID:8480181  
A/Accession: I48471  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-336 <RES>  
A/Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749  
C/Superfamily: Fc gamma receptor I; immunoglobulin homology  
C/Keywords: immunoglobulin receptor  
F:128-180/Domain: immunoglobulin homology <IMM>

Query Match 12.7%; Score 396; DB 2; Length 336;  
Best Local Similarity 36.1%; Pred.No. 2.6e-19;  
Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

Qy 3 LWVI--LLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTCKGFRFYSPQKTWYHR 60  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
10 MWLLTTLVVPGVGVEVNATKAVITLQPWSAIFQKENTLMCEGPHLPDSSSTOWFIN 69  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 61 YLGKEIURETPD---NILEVOEGEVCRCQAQGSLPSVHLDFFSSAS-LILQAPLSVF-E 115  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
70 --GTVQTSTPYSISVASPQDSGEVRCQIGSSVPDPVQLIHKEDWLILLQASRRVLTE 127  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 116 GDSVVLTRCA-KAEVTLNNTIYNNDNVLAFLNKRTDFHIPHACLKONGAYRCTG---YKE 171  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
128 GEPLALCKCHGNKNLVNVVFNKGSFKF-SGSKTIALTKNLSHSIGHCSGMGRHY 186  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 172 SCCPVSNVTVKIQOEBFTFPLVRASSFQPI-SGNPNVTLTCETQLSLERSDVPLRFRRFR 230  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
187 TSAGVSI-TVKAPLELFTPLVRASVSPFPPEGLSVTLNCETNALLQRPGLQLYSFVY 245  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 231 DDQTLGLGWLSNPQITAMWSKDSGYCKAAAMPHSVSDSPRWIQVIP-ASHPV 288  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
246 GSKILEYR-NTSEYHIARAERDAGFYWCVEATDSSVLKHSPKLEQLVLGQQSAPV 303  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::

RESULT 5

I46021  
Fc-gamma receptor II - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I46021; S4204  
R/Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.  
Immunogenetics 39, 423-427, 1994  
A>Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.  
A/Reference number: I46021; MUID:94245284; PMID:8188320  
A/Accession: I46021  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-296 <ZHA>  
A/Cross-references: UNIPROT:Q28110; EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g437978  
C/Superfamily: Fc gamma receptor III; immunoglobulin homology  
C/Keywords: immunoglobulin receptor

Query Match 10.5%; Score 326.5; DB 2; Length 296;  
Best Local Similarity 37.0%; Pred.No. 1e-14;  
Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;

Qy 1 MLWVILLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTCKGFRFYSPQKTWYHR 60  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
28 MWLLTALLFLAPVSGK-PDLPKAVTIQPAWINVLREDHVHTLTLCQTSFSAGNLTTWFEN 86  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 61 YLGKEI-LRETDPNILEV--QESGEVRCQAQGSPLSPVHLDFFSSASLILQAPLSVF-EG 116  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
87 --GSSIHTQKPYSYFRAGNSDSSVRCQEQTSLSDPVLHDVISDWLLILTPTSLVFQEG 144  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::  
Qy 117 DSVVLRCRAKAEVTLNN-TIYKNDNVLAFLNKRTDFHIPHACLKONGAYRCTGYKSCCP 175  
Db ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::

A:Molecule type: mRNA  
A:Residues: 1-57,'D','S',9-434,'A' ,436,'FL',438-449,'O',451-502,'A' ,503-792,'K',794-908,'R'  
71-2979,'H',2981-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-  
Cross-references: EMBL:X62515

R;Tryggvason, K.  
submitted to the EMBL Data Library, October 1991

A:Reference number: S77946

A:Accession: S77946

A:Molecule type: mRNA  
A:Residues: 1-57,'D','S',9-434,'A' ,436,'FL',438-449,'O',451-502,'A' ,503-792,'K',794-908,'R'  
71-2979,'H',2981-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-  
Cross-references: EMBL:X62515; NID:g929469; PIDN:CRA44373.1; PID:g929470

R;kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Gnomics 11, 389-396, 1991

A>Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g  
A:Reference number: A41059; PMID:92120660; PMID:1685141

A:Accession: A41059

A:Molecule type: mRNA  
A:Residues: 'RT',892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 '<KA2>  
Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371

R;dodge, G.R.; Kovalesky, I.; Chu, M.L.; Hassell, J.R.; McBrade, O.W.; Yi, H.F.; Ioizzo,  
Genomics 10, 673-680, 1991

A>Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular  
A:Reference number: A40306; PMID:91365376; PMID:1679749

A:Accession: A40306

A:Molecule type: mRNA  
A:Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>  
Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425

R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den  
J. Cell Biol. 109, 3199-3211, 1989

A>Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal  
anes.

A:Reference number: A33625; PMID:90078352; PMID:2687294

A:Accession: B33625

A:Molecule type: protein  
A:Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>

A:Accession: A33625

A:Molecule type: Protein  
A:Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>

A>Note: peptide potentially matches four different regions of sequence shown

C:Genetics:

A:Gene: GDB:HSPC2

A:Cross-references: GDB:126372; OMIM:142461

A:Map position: lp36.1-lp36.1

C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembra  
F;1-21/Domain: signal sequence #status predicted <SIG>  
P;22-4391/Product: perlecan #status predicted <MAI>  
P;22-193/Domain: I <DOM1>  
F;194-530/Domain: II <DOM2>  
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F;531-1676/Domain: III <DOM3>  
F;1159-1206/Domain: laminin-type EGF-like homology <LEG>  
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>  
F;1677-3686/Domain: IV <DOM4>  
F;2007-2034/Domain: transmembrane #status predicted <TRM>  
F;3687-4391/Domain: V <DOM5>  
F;3845-3880/Domain: EGF homology <EGFI>  
F;3888-3921/Domain: EGF homology <EGF>  
F;3953-4106/Domain: laminin G repeat homology <LG2>  
F;4147-4175/Domain: EGF homology <EGF2>  
F;4149-4151/Region: motor neuron attachment (L-R-E) motif  
F;4299-4303/Binding site: motor neuron attachment (L-R-E) motif  
F;65.71.76/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
E;89\_554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (cova)  
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match            9.6%     Score 299.5; DB 2; Length 4391;  
Best Local Similarity      23.5%; Predicted No. 2.le=11;  
Gap Percentages          264; Indels 117; Gaps 28;

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QY      23  PIIFLOPPMTTVOGERVTLTKGPRFFYSPOK-TKWYHRYLGKEILRETPNIL-----E 76
Db      2630 PPIRIESSPTVEGTDLNCVWAR--QPQAIIWYKGGSLPSRQHGTGSHRLHOMS 2687
QY      77  VOBSEGYRCQAQ-----GSP---LSSPHLDFFSASLILQAPLSVF 114
Db      2688 VADSGEVCRANNIDALEASIVISVSPAGSPSAPGSSMPRIRESS-----HVA 2739
QY      115 EGDVVULRCRAAEVTNNTIYKDNVLA--FLNKRTDFHIPHACIKONGAYRC-----T 167
Db      2740 EGSTDLNLCVVPQOAHQAQVTHWKRGSLPSHHQTRGSRLLRHVSPADSGEYVCVRMGSS 2799
QY      168 GYKESCCPV---SSNTVKIQVOEPFTRPVL-ASFQPIGNPVTITC-----ETOLS 216
Db      2800 GPLEASVLVTIEASGSAHVHPAPGCGAPPRIEPSRSSRVAEQOTLDLKCVPGQHAQVT 2859
QY      217 LER--SDVPLRFRRDDQTGLGWSLSNFQITAMWKSDFYMKCK----AATPHSV- 269
Db      2860 WHKRGNLPAHQVH-----GPLRLNQVSPADSGEYSCQVTSQTTLEASVL 2907
QY      270 ISDSPRSWIOVIPASHPVLTLTSPEKALNPFGTKVTLHCETQBDLSRTLRFVHEG--VP 327
Db      2908 VTIEPSPGPIPAPGLAQPIVIEASSSHVTEGTDLNLCVVPQOA-HAQVTWYKGGSLP 2966
QY      328 LRHSKVCERCASISFSLT--ENSGNYCYCTADNGLGAKPKAYSLSVTPVSH-----379
Db      2967 ARHOT----HGSQLRLHLVSPADSGEYVCRAASGPG--PEQEAFTVTPVPPSEGSSYRLR 3020
QY      380 -PVLNLGSPEDLIPEGAKVTLHCEAQRGSPLIYQFHEDAALERSANSAGVAISFSL 438
Db      3021 SPVISIDPPSSVTVOGQDASKFKLIHDGAAPISLEWKTRNOELEDNVHISPNGSIITVG 3080
QY      439 T-AEHSGNYCYCTADNGFGPQRSKAVALSITVPVSHPVLTLSSAEALTFEGATVTLHCEVQ 497
Db      3081 TRPNSNHGTYRCVASNAVQAQS-VVNLSVHGPPPT--VSUPLPEGVPVVKVKAVTEC-VS 3136
QY      498 RGSPOILYQFYHEDMPLVSSSTPVSGRVSFSFSLITEGH-----SGNYCYCTADN 545
Db      3137 AGEPRSSARWR-----ISSTPA-KLEORTYGLMDSHAVALQISSAKPESDAGTVCLCAQN 3189
QY      546 GFQPORSSEVVSFLVTFG 561
Db      3190 ALGTAQKQVEIVIDTG 3205

```

RESULT 8  
JL0107

Fc gamma (19G) receptor III-A precursor (natural killer cell) [validated] - human  
 JLO107  
 N:Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surfactant protein 1  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Sep-1990 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: JLO107; A60383; A32933; I37627  
 R:Ravetch, J. V.; Perussia, B.  
 J. Exp. Med. 170, 481-497, 1989  
 A:Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cells  
 A:Reference number: JLO107; PMID:89328325; PMID:2526846  
 A:Accession: JLO107  
 A:Molecule type: mRNA  
 A:Residues: 1-254 <RAW>  
 A:Cross-references: UNIPROT:P08637; GB:X52645; GB:M31937; NID:931323; PIDN:CRA36870.1; PDB:1A00  
 A:Note: the sequence of the receptor from human polymorphonuclear granulocytes, reported by the authors, differs from the sequence of the receptor from human neutrophils by 21 residues  
 21 residues  
 R:Trounstein, M.L.; Peltz, G.A.; Yssel, H.; Huizinga, T.W.J.; von dem Borne, A.E.G.K.; Staal, G.E.  
 Int. Immunol. 2, 303-310, 1990  
 A:Title: Reactivity of cloned, expressed human Fc gamma RIII isoforms with monoclonal anti-CD16 antibodies  
 A:Reference number: A60383; MUID:91120527; PMID:1703781  
 A:Accession: A60383  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-254 <TRO>  
 R:Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.  
 J. Exp. Med. 166, 5079-5083, 1989

[illegible]

Thu May 5 15:10:59 2005

```

RESULT 10
S06946
Fc gamma (IgG) receptor - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: S06946
R:Stuart, S.G.; Simister, N.E.; Clarkson, S.B.; Kacinski, B.M.; Shapiro, M.; Mellman, I.
EMBO J. 8, 3657-3666, 1989
A:Title: Human IgG Fc receptor (hFCRII; CD32) exists as multiple isoforms in macrophages
A:Reference number: S06946; MUID:90059965; PMID:2531080
A:Accession: S06946
A:Molecule type: mRNA
A:Residues: 1-333 <STU>
A:Cross-references: UNIPROT:P31995; EMBL:X17652; NID:G32073; PIDN:CAA35642.1; PID:G32074
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:64-115/Domain: immunoglobulin homology <IMM>

Query Match 9.3%; Score 290; DB 2; Length 323;
Best Local Similarity 36.3%; Pred. No. 3.2e-12;
Matches 74; Conservative 26; Mismatches 84; Indels 20; Gaps 6;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 28 MLLWTVLFLAPVAGTPAAPPKAVLKLEPQWINVQLQSDSVTLTCRGTSPESDSIQWFHN 87
QY 61 YLGEILRETPDNI---LEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTQPSYRFKANNNDSEYTCQTGTSLSDPVHLTVLSEWLVLTQPHLEFQEG 145
QY 117 DSVVLCRA-KAEVTLNNTIYKNDNLVLAFLNKTDFHPIHACLKONGAYRCTG-----Y 169
DB 146 ETIVLRCHSWKDKPLVKVTFQNGSKKFSRSDPNFSIPQANHSHSGDYHCTGNGITYLY 205
QY 170 KESCCPVSSNTVKIQVQEPTRPV 193
DB 206 -----SSKPEVTITVQAPSSSPM 222

RESULT 11
JL0119
Fc gamma (IgG) receptor IIB precursor - human
A:Alternate names: Fc gamma (IgG) receptor II (low affinity) beta; surface glycoprotein
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JL0119; A43543; A60568; A45877; S00478
R:Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
A:Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
A:Reference number: JL0119; MUID:90010791; PMID:2529342
A:Accession: JL0119
A:Molecule type: mRNA
A:Residues: 1-310 <BRO>
A:Cross-references: UNIPROT:P31994
R:Engelhardt, W.; Geerts, C.; Frey, J.
Eur. J. Immunol. 20, 1367-1377, 1990
A:Title: Distribution, inducibility and biological function of the cloned and expressed
A:Reference number: A43543; MUID:90316181; PMID:2142460
A:Accession: A43543
A:Molecule type: mRNA
A:Residues: 1-204, 'Y', 206-254, 274-310 <ENG>
A:Cross-references: GB:X52473; NID:G3928171; PIDN:CAA36713.1; PID:G29428
R:Engelhardt, W.; Geerts, C.; Frey, J.
Mol. Immunol. 27, 379-382, 1990
A:Title: Organization of human FcRII and FcRII-like (betaFCRII) genes: structural homolo
A:Reference number: A60568; MUID:90294837; PMID:2141667
A:Accession: A60568
A:Molecule type: DNA
A:Residues: 1-38 <EN2>
R:Seki, T.
Immunogenetics 30, 5-12, 1989
A:Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
A:Reference number: A45877; MUID:89307398; PMID:2526077
```

```

A:Accession: A45877
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-74, 'Q', 76-119, 'V', 121-204, 'Y', 206-231, 'T', 233-254, 274-310 <SEK>
A:Cross-references: GB:M28696; NID:G184843; PIDN:AAA36051.1; PID:G306929
A:Note: the authors translated the codon CAG for residue 75 as His
R:Stengelin, S.; Stamenkovic, I.; Seed, B.
EMBO J. 7, 1053-1059, 1988
A:Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity clonin
A:Reference number: S00477; MUID:88296409; PMID:3402431
A:Accession: S00478
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-35, 'S', 37-204, 'Y', 206-253, 'G', 255 <STE>
A:Note: the authors suggest that the cDNA is derived from a precursor RNA that still cont
C:Genetics:
A:Gene: GDB:FCGR2B; FCG2; FCGR2
A:Cross-references: GDB:128183; OMIM:146790
A:Map position: 1q23-1q23
A:Introns: 131/1
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin; immunoglobulin receptor;
F:1-44/Domain: signal sequence #status predicted <SIG>
F:45-310/Product: IgG Fc receptor IIB #status predicted <MAT>
F:45-222/Domain: extracellular #status predicted <EXT>
F:64-115/Domain: immunoglobulin homology <IMM1>
F:145-198/Domain: immunoglobulin homology <IMM2>
F:223-245/Domain: transmembrane #status predicted <TMM>
F:246-310/Domain: intracellular #status predicted <INT>
F:246,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Query Match 9.3%; Score 289; DB 2; Length 310;
Best Local Similarity 36.9%; Pred. No. 3.8e-12;
Matches 73; Conservative 26; Mismatches 91; Indels 8; Gaps 5;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 28 MLLWTVLFLAPVAGTPAAPPKAVLKLEPQWINVQLQSDSVTLTCRGTSPESDSIQWFHN 87
QY 61 YLGEILRETPDNI---LEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTQPSYRFKANNNDSEYTCQTGTSLSDPVHLTVLSEWLVLTQPHLEFQEG 145
QY 117 DSVVLCRA-KAEVTLNNTIYKNDNLVLAFLNKTDFHPIHACLKONGAYRCTG-----Y 175
DB 146 ETIVLRCHSWKDKPLVKVTFQNGSKKFSRSDPNFSIPQANHSHSGDYHCTG-NIGYTL 204
QY 176 VSSNTVKIQVQEPTRPV 193
DB 205 FSSKPEVTITVQAPSSSPM 222
```

```

RESULT 12
I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:G1017426; PIDN:CAA62189.1; PID:G101
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 8.8%; Score 275; DB 2; Length 7962;
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Best Local Similarity 25.0%; Pred. No. 2e-09;  
Matches 150; Conservative 71; Mismatches 262; Indels 116; Gaps 27;

Qy 23 PIIFLQPPWTVFQGERVLTLC-----KGFRFYSPQKTWKVHYRLYGKILRE 69  
Db 216 PTFLSRPSKSLTFVCKAAKFCITVGTGVETIWDGGAALSPNWRISDAENKHILEL 275

Qy 70 TPDNILEVQESGEYRCQAGSPSLSPVHLDFSASLIL-----OAPLSVFEQDSVV 120  
Db 276 SN---LTIQDRGVYSCKA-----SNKFGADICQAEILIIDKPHFIKELEFPVQSAINKKVH 327

Qy 121 LRCRA-----KAEVTLNNIYK-----NDNVLAFLNKGTDFHIIACUKDNGAVRCTGYKGS 172  
Db 328 LECQVDEDRKVTVTWSKDGQKLPGPKDYKICFEDKIATLEIPLAKLKDGGTYVCTASNEA 387

Qy 173 CPGVSSNTVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTETQLTSLSRSDVPLRFRFRDD 232  
Db 388 GSSSCSAVTTVREPPSFVKVK---DPSYLMPLGESAKLHCK----LKGSPV-IQVTFWKNN 440

Qy 233 QTLGLGWSLSPNF-----QITAMWSKDSGFYWCNKAATMPSHVSIDSPPRSWIQVOIPAS 285  
Db 441 KELSESNTVMYFVNSEALDITDVKVEDSGSYSCAV---NDVSGDS-CSTEIVIKPEPS 497

Qy 286 HPVLTLSPEKALNFGTKVTLHCET-----QEDSLRT--LYRPFYHEGVPLRHK 331  
Db 498 F-IKTLPEADIV--RGTNALLQCEVSGTGPFPEISWFKDKKQIRSSKKYRLFQ-----K 548

Qy 332 SVRCERGASISFSLTTEGNSNYCTADNCLGAKPKSAVSLSTVTVPSHVLNLSPPEDLI 391  
Db 549 SLVCLD-----IPSFNSADVGEYECVAVNEVGKCGCMATHL-----LKBPPTTFVKKVDLLI 599

Qy 392 PEGAKVTILHCEAQRGLPIL-----YOPHHDEAALERRSANSAGGVAISF--SLTAEHS 443  
Db 600 ALGGQVTVLQAAVRGSEPISVTMWKGQEVIREDGKIKMSFSN---GVAVLIIPDVQISFG 656

Qy 444 GNYCTADNGFGPQRSKAVSLITVPVSHVLTLSAEAL-TFEGATVTLHCEVQRGSPQ 502  
Db 657 GKYTCLAEAGSQTSGVELI-----VKPEAKIIERAELIQVTAGDPATLETV-AGTPE 710

Qy 503 ILYOFYHEDMPLVSSSTSGVRVSF-----SFSLTEGH-SGNYCYCTADNGFGPQSE 553  
Db 711 LKPRWKDGRPLVAASK---YRISFPNNVAUKFYSAELHSDGQYTFEISNEVGSSC 766

RESULT 13  
JC7593

SH2 domain-containing phosphatase anchor protein la - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C/Accession: JC7593  
R/Xu, M.; Zhao, R.; Zhao, Z.J.  
Biochem. Biophys. Res. Commun. 280, 768-775, 2001  
A/Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.  
A/Reference number: JC7593; MUID:21092675; PMID:11162587  
A/Accession: JC7593  
A/Molecule type: mRNA  
A/Residues: 1-255 <XUA>  
A/Cross-references: UNIPROT:Q9B2I6; GB:AF319438  
C/Genetics:  
A/Map position: 1q21  
A/Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3  
C/Keywords: glycoprotein  
F/27-135/Domain: extracellular #status predicted <EXT>  
F/68-115/Domain: immunoglobulin-like #status predicted <IGL>  
F/148-169/Domain: transmembrane region #status predicted <TMM>  
F/195-255/Domain: intracellular #status predicted <INT>

Query Match 8.7%; Score 272; DB 2; Length 255;  
Best Local Similarity 57.6%; Pred. No. 3.8e-11;  
Matches 57; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

Qy 371 LSVTVPSVSHPVNLSSPEDLIPEGAKVTLHCEAQRGLPILYOFHDEAALERRSANSAG 430



us-09-724-254a-3.rpr

Thu May 5 15:10:59 2005

C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004  
 A:Accession: J10118; A31932; S02297; B45877; S00477; S02296  
 R:Brooks, D.G.; Qiu, W.O.; Luster, A.D.; Ravetch, J.V.  
 J. Exp. Med. 170, 1369-1385, 1989  
 A>Title: Structure and expression of human IgG FcRII(CD32): functional heterogeneity is  
 A:Reference number: J10118; PMID:90010791; PMID:2529342  
 A:Accession: J10118  
 A:Molecule type: mRNA  
 A:Residues: 1-317 <BR>  
 A:Cross-references: UNIPROT:P12318; GB:M31932; NID:g182473; PIDN:AAA35827.1; PID:g182474  
 A:Experimental source: placenta  
 A>Note: it is uncertain whether Met-1, Met-3, or Met-7 is the initiator  
 R:Hibbs, M.L.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarth, P.M.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2240-2244, 1988  
 A>Title: Molecular cloning of a human immunoglobulin G Fc receptor.  
 A:Reference number: S02296; PMID:88176920; PMID:2965389  
 A:Accession: A31932  
 A:Molecule type: mRNA  
 A:Residues: 1-317 <HIB>  
 A:Cross-references: EMBL:J03619; NID:g183619; PIDN:AAA35932.1; PID:g306803  
 R:Stuart, S.G.; Iroustine, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; Mc  
 J. Exp. Med. 166, 1668-1684, 1987  
 A>Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-  
 A:Reference number: S02297; PMID:88061079; PMID:2824655  
 A:Accession: S02297  
 A:Molecule type: mRNA  
 A:Residues: 1, 'T', 3-317 <STU>  
 A:Cross-references: EMBL:Y00644; NID:g31335; PIDN:CAA68672.1; PID:g31336  
 A>Note: it is uncertain whether Met-1 or Met-7 is the initiator  
 R:Seiki, T.  
 Immunogenetics 30, 5-12, 1989  
 A>Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.  
 A:Reference number: A45877; PMID:89307398; PMID:2526077  
 A:Accession: B45877  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 7-317 <SEK>  
 A:Cross-references: GB:M28697; NID:g184841; PIDN:AAA36050.1; PID:g306928  
 R:Stengelin, S.; Stamenkovic, I.; Seed, B.  
 EMBO J. 7, 1053-1059, 1988  
 A>Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity cloni  
 A:Reference number: S00477; PMID:88296409; PMID:3402431  
 A:Contents: clone PC23  
 A:Accession: S00477  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 7-317 <STE>  
 C:Genetics:  
 A:Gene: GDB:FCGR2A  
 A:Cross-references: GDB:119903; OMIM:146790  
 A:Map position: 1q23-1q23  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:36-317/Product: IgG Fc receptor Iia #status predicted <REI>  
 F:36-216/Domain: extracellular #status predicted <EXT>  
 F:36-216/Domain: immunoglobulin homology <IMM1>  
 F:36-106/Domain: immunoglobulin homology <IMM2>  
 F:136-189/Domain: transmembrane #status predicted <TMM>  
 F:217-240/Domain: intracellular #status predicted <INT>  
 F:241-317/Domain: intracellular #status predicted <INT>  
 F:97,178/Binding site: carbohydrate (Asn) #status predicted

Query Match 8.5%; Score 264.5; DB 2; Length 317;  
 Best Local Similarity 35.7%; Pred. No. 1.6e-10;  
 Matches 70; Conservative 25; Mismatches 88; Indels 13; Gaps 6;  
 QY 3 LWV-----ILLVLAPVSGQPARTPRPIIFLQPPWTVTFQGERVTLTKGFRFYSQKTKW 57  
 Db 16 LMLQLPLTVLLLASADSQAAPKVKLEPPINVLQEDSVTLTCQARSFSDSIQW 75  
 QY 58 YHYLKGKELLRETPDNI---LEVQESGEYRCQAQSGPLSPVHLDPFSSASLIQAP-LSV 113  
 Db 76 FHN--GNLIPHTQPSYRFKANNNDSEYTCQTGTSLSDDPVHLTVLSEWLVLTQPHLEF 133

QY 114 FEGDSVLRCA-KAEVTIANNTIYKNDNLAFINKRTDFHPIHACLKNDGAYRCTGYKES 172  
 Db 134 QEGETIMLRCHSWKDKPLVKVTFQNGKSKQFSLDPTFSIPQANHSHSGDYHCTG-NIG 192  
 QY 173 CCPVSSNTVKIQVQBP 188  
 Db 193 YTLFSSKPVTVITVQVP 208

Search completed: May 4, 2005, 11:39:18  
 Job time : 20.5636 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 79.8488 Seconds  
(without alignments)  
3796.562 Million cell updates/sec

Title: US-09-724-254A-3  
Perfect score: 3124  
Sequence: 1 MLLWVILLVLPVSGQFART.....AEFSLTHSFKNLFALESFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2949	94.4	977	2 Q96RD9	Q96RD9 homo sapien
2	1193.5	38.2	734	2 Q96LA4	Q96LA4 homo sapien
3	1193.5	38.2	734	2 Q96P31	Q96P31 homo sapien
4	1193.5	38.2	742	2 Q8NGS2	Q8NGS2 homo sapien
5	1186.5	38.0	740	2 Q96P29	Q96P29 homo sapien
6	927.5	29.7	582	2 Q80WN2	Q80WN2 mus musculus
7	927.5	29.7	595	2 Q68SN8	Q68SN8 mus musculus
8	847.5	27.1	639	2 Q96P30	Q96P30 homo sapien
9	826.5	26.5	515	2 Q96P75	Q96P75 homo sapien
10	820.5	26.3	515	2 Q96RE0	Q96RE0 homo sapien
11	773.5	24.8	508	2 Q96LA5	Q96LA5 homo sapien
12	772	24.7	360	2 Q8N732	Q8N732 homo sapien
13	692.5	22.2	508	2 Q8BJA5	Q8BJA5 mus musculus
14	657.5	21.0	437	2 Q8NF56	Q8NF56 homo sapien
15	600.5	19.2	509	2 Q9EQV5	Q9EQV5 m musan-g pr
16	599.5	19.2	509	2 Q91VK7	Q91VK7 mus musculus
17	565	18.1	428	2 Q96P36	Q96P36 homo sapien
18	565	18.1	429	2 Q96LA6	Q96LA6 homo sapien
19	548	17.5	124	2 Q6UY46	Q6UY46 homo sapien
20	548	17.5	366	2 Q8N759	Q8N759 homo sapien
21	543.5	17.4	154	2 Q8N733	Q8N733 homo sapien
22	537.5	17.2	422	2 Q96P33	Q96P33 homo sapien
23	452	14.5	722	2 Q6GNB3	Q6GNB3 xenopus lae
24	448.5	14.4	426	2 Q6BAA4	Q6BAA4 homo sapien
25	446.5	14.3	626	2 Q6DCH3	Q6DCH3 xenopus lae
26	428.5	13.7	357	2 Q8SPW5	Q8SPW5 macaca fasc
27	418.5	13.4	374	1 FCGL HUMAN	P12314 homo sapien
28	402.5	12.9	372	2 Q7YQJ5	Q7YQJ5 canis famil
29	402.5	12.9	404	1 FCGJ_MOUSE	P26151 mus musculus
30	396	12.7	330	2 Q8R142	Q8R142 mus musculus
31	369	11.8	349	2 Q9M2T0	Q9M2T0 bos taurus

32	343	11.0	208	2 Q80WN3	Q80WN3 mus musculus
33	342	10.9	413	2 Q6ZNI1	Q6ZNI1 homo sapien
34	340	10.9	300	2 Q68SP0	Q68SP0 mus musculus
35	340	10.9	434	2 Q6DN72	Q6DN72 homo sapien
36	339	10.9	275	2 Q6BAA1	Q6BAA1 homo sapien
37	338	10.8	324	2 Q7TMH2	Q7TMH2 mus musculus
38	338	10.8	343	2 Q8R4Y0	Q8R4Y0 mus musculus
39	337	10.8	343	2 Q8BYS4	Q8BYS4 mus musculus
40	332.5	10.6	359	2 Q7LS13	Q7LS13 homo sapien
41	332.5	10.6	365	2 Q8NEW4	Q8NEW4 homo sapien
42	332.5	10.6	376	2 Q8WXH3	Q8WXH3 homo sapien
43	330	10.6	397	2 Q6XRC3	Q6XRC3 homo sapien
44	326.5	10.5	296	1 FCG2_BOVIN	Q28110 bos taurus
45	326.5	10.5	318	2 Q6BAA3	Q6BAA3 homo sapien

ALIGNMENTS

RESULT 1  
Q96RD9 ID Q96RD9 PRELIMINARY; PRT; 977 AA.  
AC Q96RD9, AC Q96RD9, PRT; 977 AA.  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE FC receptor-like protein 5.  
GN Name=FCRH5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396552; PubMed=11493702; DOI=10.1073/pnas.171308498;  
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;  
RT "Identification of a family of Fc receptor homologs with preferential  
RT B cell expression."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).  
DR EMBL; AF397453; AAK93971.1; -.  
DR HSSP; P12319; 1F2Q.  
DR GO; GO:0004872; Fireceptor activity; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; PF00047; Ig; 8.  
DR SMART; SM00408; IgC2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 8.  
KW Receptor.  
SQ SEQUENCE 977 AA; 106496 MW; 24BA027B25509E7 CRC64;

Query Match 94.4%; Score 2949; DB 2; Length 977;  
Best Local Similarity 98.3%; Pred. No. 4.6e-204;  
Matches 562; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60
DB	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVFEQDSVV	120
DB	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVFEQDSVV	120
QY	121	LRCKRAEYTLNNTIYKNDNVLAFLNKRITDFHIFHACLKNDGAYRCTGYKESCCPVSSNT	180
DB	121	LRCKRAEYTLNNTIYKNDNVLAFLNKRITDFHIFHACLKNDGAYRCTGYKESCCPVSSNT	180
QY	181	VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLFRFRFRDDDTGLGWS	240
DB	181	VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLFRFRFRDDDTGLGWS	240
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKALNFE	300
DB	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKALNFE	300

Db	177	TSKPLNIQVLEFLHPLVRASSSTPIEGSPMTLTCETQLSPQRPDVOLQFSLFRDSQTLG	236
Qy	237	LGWSLSPNQITAMSKSDGFFVCKAAAMPHSVISDSPRSWIQVO-IPASHPVLTLSPEK	295
Db	237	LGWSRSPRLQIPAMWTEDSGVCWEVETVTHSIKKRSLRQIRQVRVPVSVNVLEIRPTG	296
Qy	296	ALNFEGTKVTLHCETOEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTT---ENSGN	352
Db	297	GQLIEGNMVLICSVAQSGSTVPSWHKEG-RVRSGLRKTQRSLLAEHLVLTVKESDAGR	355
Qy	353	YYCTADNGLGAKESKAVSLSVTPVPSHVLNLSPPEDLIPEGKVTLHCEAQRGSPLILY	412
Db	356	YYCAADNVHPILSTWIRVTIRIPVSHPVLTFRAPRAHTVVGDDLELHCSLGRGSPILY	415
Qy	413	QPHHEDAAALERRANSAGGVALSFSILTAHSGNYCYCTADNFGFQPSKAVSLGTTVPVSH	472
Db	416	RFYHEDVTLGNSAPGGGGASFNLSUTAEHSGNYSCDADNGLGHQHGSHGSLRVTVPSR	475
Qy	473	PVLTLSAEALTFEGATVTLHCEVORGSPQILLYQFYHEDMPLVSGSSPTPSVGRVSFSLSL	532
Db	476	PVLTIRAPGAQVVGDDLELHCSLRGSPILYWFYHEDDTLGNISAHSGGGASFNLSLT	535
Qy	533	EGHSGNYCYCTADNFGFQPSREVVSLFVTG	561
Db	536	TEHSGNYSCDADNGLGHQHGSKVYTLNVTG	564

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RESULT 3
Q96FP31 PRELIMINARY; PRT; 73A AA.
ID Q96P31
AC Q96P31;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DC 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 26, Last annotation update)
DI 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
Xu M.-J., Zhao R., Zhao Z.J.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF416901; AAL13290.1; -.
DR HSP; PI2319; 1F2Q.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; 1.
DR PROSITE; PS00092; N6_MTASE; 1.

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Query Match	38.2%;	Score 1193.5;	DB 2;	Length 734;	
Beat Local Similarity	45.5%;	Pred. No. 1.7e-7;			7
Matches 259;	Conservative 76;	Mismatches 221;	Indels 13;	Gaps	
QY	1	MLLWVILLVLAPVSGQFARTPPRIIFLPQPTWTFQGERVLTCKGGRFFYSPO-KTKWYH	59		
Db	1	MLLWLLILLITPCREQSGVAPKAVLLAPPMTSTAFKKEKVALICSSISHSLAODTIWYH	60		
QY	60	RYLCKEILRETDPNILEVOESGEYRCOAQGPLSPVHLDFFSSASLIQLAPLGVFEGDSV	119		
Db	61	---DEKLLIKTKHDKI-QITTEPGNYCCKIRFGSLSDAVHVEFSPDWLLILQALHPVFE	116		
QY	120	VLRCKRAEAVTLNNTIYKNDNLVLAFLNKRTDPIHIIHACLKONGAYRCGTGKESC--	176		
Db	117	ILRCQGDKNKNTHQKVYKDGKGLPMSYNLEKITVNSVSRDNSKYCHCTAYAKFTILDIEV	176		
QY	177	SSNTVKIQVEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPRLRFFRDDDTLIG	236		
Db	177	TSKPLINTQVQELFHLHPVLRASSSTPTPEGSPWILTCTQLSPQRPDVQLQFSLFRDSOTLIG	236		

301	QY	GTQVTLHCETOEDSLRTLYRPHYHGVPLRHKSVCRCGASISFSLTTENGSGNYCTADNG	360
301	Db	GTQVTLHCETOEDSLRTLYRPHYHGVPLRHKSVCRCGASISFSLTTENGSGNYCTADNG	360
361	QY	LGAKPSKAVLSVTVPVSHVPLNLSPPEDLI FEGAKVTLHC EAQRGSLPILYQPHHEDAA	420
361	Db	LGAKPSKAVLSVTVPVSHVPLNLSPPEDLI FEGAKVTLHC EAQRGSLPILYQPHHEDAA	420
421	QY	LERRANSAGGVAISFSLTAESHGNYCTANGFGPQRSKAVLSITVPVSHPVLTLSA	480
421	Db	LERRANSAGGVAISFSLTAESHGNYCTANGFGPQRSKAVLSITVPVSHPVLTLSA	480
481	QY	EALTEGATVTLHCEVQRGSPQILYQFVHEDMPLVSSSTPSVGRVSRFSFSLTEHSGNYY	540
481	Db	EALTEGATVTLHCEVQRGSPQILYQFVHEDMPLVSSSTPSVGRVSRFSFSLTEHSGNYY	540
541	QY	CTADNGFGPQRSEVVSFLFVTGKCVLASKPPL	572
541	Db	CTADNGFGPQRSEVVSFLFVT----VPVSRPIL	568

RESULT 2  
95951A4

AC	01-DRC-2001	(T-EMBLrel. 19, Created)
AD	01-DRC-2001	(T-EMBLrel. 19, Last sequence update)
AE	01-DRC-2001	(T-EMBLrel. 19, Last sequence update)
AF	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)
AG	FC	receptor-like protein 3.
AH	FC	receptor-like protein 3.
AI	Name=FCRH3;	
AJ	OS	Homo sapiens (Human).
AK	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AL	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AM	OC	
AN	NCBI_TaxID=9606;	
AO	[1]	
AP	SEQUENCE=395652.	
AQ	MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;	
AR	Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;	
AS	"Identification of a family of Fc receptor homologs with preferential	
AT	B cell expression.";	
AV	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).	
AW	EMBL; AY043466; AAK91779.1; -	
AX	HSP; P12319; 1F20.	
AY	GO; GO:0004872; F:receptor activity; IEA.	
AZ	InterPro; IPR007110; Ig-like.	
BA	InterPro; IPR003598; Ig_c2.	
BB	InterPro; IPR002052; N6_Mcase.	
BC	Pfam; PF00047; Ig; 4.	
BD	SMART; SM00408; IGC2; 1.	
BE	PROSITE; PS50835; IG_LIKE; 6.	
BF	PROSITE; PS50835; N6_Mcase; UNKNOWN 1.	

[illegible]



DR PROSITE; PS00835; IG LIKE; 6.  
DR PROSITE; PS00092; N6\_WTASE; UNKNOWN 1.  
SQ SEQUENCE 740 AA; 81440 MW; 038AFa83A2909E46 CRC64;  
Query Match 38.0%; Score 1186.5; DB 2; Length 740;  
Best Local Similarity 45.2%; Pred. No. 5.4e-77;  
Matches 260; Conservative 75; Mismatches 221; Indels 19; Gaps 8;  
QY 1 MLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFGSERVTLTCKGFRFYSPQ-KTKWYH 59  
DB 1 MLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFGSERVTLTCKGFRFYSPQ-KTKWYH 60  
QY 60 RYLKGLREITPDNILEVQESGEYRCQAGSPSSPLSPVHLDFSSASLILOAPLSVPEGDSV 119  
DB 61 ---DEKLKIKHKDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVPEGDNV 116  
QY 120 VLRCRAKAEVTLNNTYKNDVLAFLNKETDHPHACLKONGAYRCTGYKESC---CPV 176  
DB 117 ILRCQKDNKNTKQYKYYKDGKQLPNYNLEKITVNSVSRDMSKYHCTAYRKFYILDIEV 176  
QY 177 SNTVTKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLG 236  
DB 177 TSXPLNIQVQLFLHPLVRASSSTPIEGSPMTLTCTQLSPQRPDVLQFSLFRDSQTLG 236  
QY 237 LGWSLSPNFQITAMWSDGFGFYCKAATMPHVSIDSPSRWIQVQ-IPASHPVLTLSPK 295  
DB 237 LGWSRSPRLQIPAMWTDSDGSYWCVEYVTHSIKKRSLRSQIRVQRPVSNVNLIRPTG 296  
QY 296 ALNFEQTKVTLHCETQEDSLRTLYRYFHEGVPLRHKSVCRCGASISFSLTT---ENSGN 352  
DB 297 GQIEGNNVLLICSVAGSGSTVTFVSHKEG-RVRSIGRKTQSRLLAELHLVTLVKESDAGR 355  
QY 353 YYCTADN-----GLGAKPKAVSLSVTVVSHPVNLNLSPEDLIPEGAKVTLHCEAQRG 406  
DB 356 YYCAADNVHSPILSTWIRVTVTLTLLSPVSHPVLTFRAPRAHTVVGDLLELHCESLRG 415  
QY 407 SLPLIYOFHEDHAALERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLGI 466  
DB 416 SPPLIYRYFHEVDTLGNSSAPSGGGASFNLSLTAHSGNYYCTADNGLGAQSHGVSLRV 475  
QY 467 TVPVSHPVLTLSAEALTPEGATVTLHCEVQGRSPQILYOFYHEDMPLVSSSTPPSVGRVS 526  
DB 476 TVPVSRLVTLRAGAAVGDLELHCESLRGSPILYWFYHEDDTLGNISAHSGGGAS 535  
QY 527 FFSLSLTHSGNYYCTADNGFGPQRSEVSLFTVG 561  
DB 536 FNLSLTHSGNYSCEADNGLGAQSHKVTLNVTG 570  
RESULT 6  
Q80WN2 PRELIMINARY; PRT; 582 AA.  
ID Q80WN2  
AC Q80WN2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE EXWASI-like protein 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Nakayama Y., Maher S.E., Weissman S.M., Bothwell A.L.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY158090; AAO20873.1; -;  
DR HSP; P12319; 1F2Q.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00408; IGc2; 2.  
DR PROSITE; PS00835; IG LIKE; 5.  
SQ SEQUENCE 582 AA; 65248 MW; 44321E93FB9EDF06 CRC64;  
Query Match 29.7%; Score 927.5; DB 2; Length 582;  
Best Local Similarity 41.9%; Pred. No. 2e-58;  
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;  
QY 3 LWLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFGSERVTLTCKGFRFYSPQKTKWYHRL 62  
DB 1 MWLWLLVLAIVSGQFARTPRPIIFLOPPWTTVFGSERVTLTCKGFRFYSPQKTKWYHRL 62  
QY 63 GKELRETPD-----NILEVQESGEYRCQAGSPSSPLSPVHLDFSSASLILOAPLSVFE 116  
DB 59 -RKTVKQTPCALVIKHAHLKVESGEYWCQADSLPFSMHVNVFSEDFVLQAPPAVFE 117  
QY 117 DSVLRCRAKAEVTLNNTYKNDVLAFLNKETDHPHACLKONGAYRCTGYKESC--- 173  
DB 118 DSVLRCYAKKGEAEATLTFYKQKALT-LHGOSELSIHANLKNGOYKCTSKKWSFG 176  
QY 174 CPVSSNTVTKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLRFRFRDDQ 233  
DB 177 SLYTSNTVGVQVQLFPRPVLRARPSHPIDGSPVTLTCTQLSAQKSDARLQCFPRNLQ 236  
QY 234 TLGLGWSLSPNFQITAMWSDGFGFYCKAATMPHVSIDSPSRWIQVQIPASHPVLTLSP 293  
DB 237 LLGSGCSRSEFHHIPAIWTEESRRYOCKAETVNSQVRKQSTAFIIPVORASAPFTHIIP 296  
QY 294 EKALNFEQTKVTLHCETQEDSLRTLYRYFHEGVPLRHKSVCRCGASIS 342  
DB 297 ASKLVFEGQLLLNCV-----KGVPGLKFSWKYKMDLNEETKILKSSNAE 343  
QY 343 FSLTATEN---SGNYCTADNGLGAKPKAVSLSVTVVSHPVNLNLSPEDLIPEGAKVTL 399  
DB 344 FKISQWNISDAGEVHCATNSRRSFVSRAFPITIKVPVQFVLTSTGKTALEGLDMLT 403  
QY 400 HCEAQRGSLPLIYOFHEDHAALERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQR 459  
DB 404 HCQQRGSPCLYBFFYENVSLGNSSILSGGCAVFNFSMSTERSGNYCTADNGLGAQCS 463  
QY 460 KAVLSLI-----TVPVS 471  
DB 464 EAIRISIFDMTKNSRVPMA 482  
RESULT 7  
Q68SN8 PRELIMINARY; PRT; 595 AA.  
ID Q68SN8  
AC Q68SN8;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Fc receptor-like protein 3.  
GN Name=Fcr3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Spleen;  
RX PubMed=15302849;  
RA Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;  
RL "Differential B cell expression of mouse Fc receptor homologs";  
RT Int. Immunol. 16:1343-1353(2004).  
DR EMBL; AY506558; AAS91578.1; -;  
DR GO; GO:0004872; Fc receptor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00409; IG; 5.  
DR SMART; SM00408; IGc2; 4.  
DR PROSITE; PS50835; IG LIKE; 5.  
KW Receptor.

[illegible]

Db	61	HTWGEKLTITPGNTLEVRSGLYRCQARGSPRNPVRLTFSSDSLLOAPYSVFEGLTV	120
Qy	121	LRCKRAEAVTLNNTYK-NDNVIAFLNKRTPHACLKONGAYRCTGYKESCCPVSSN	179
Db	121	LRCHRRRKEKLTAVKYTWNGNLTLSNKSVDLLIPQASNNNGNRCICYGENDVFRLN	180
Qy	180	TVKIQVOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVLPFRFFRDDQTLGLGW	239
Db	181	FKIIKIQELFPPHPELKATDSQTEGNSVNLSCETQLPPERSDTPLFHFNFRDGEVILSDW	240
Qy	240	SLSNPFQITAMWSKSGFYWCXAAATPHSVISDSPRSWIQV-IPASHPVLTLSPKALN	298
Db	241	STYPELQLPTVWRENSGSYWCAGETVRGNIHKHSPSLQIHVORI	300
Qy	299	FEKTKVTLHCEETOEDSLRTLYRPFYHEGV-PLRHKSVCRCERGASISFSLTTENSNNYCT	356
Db	301	VEGEMLVLCVSAEGTDTFFSHREDMQESLGRKTQSLRAELELPAIROSHAGGYCT	360
Qy	357	ADNGLGAKPSKAVSLSVTVFVSHPVNLSPEDLIFEQA-----KVTLLHCEAQ	404
Db	361	ADNSYG--PVQSMVNLVTVRETP-----GNRDGLVAAGATGGLLSALLLAVALLFHCWRR	413
Qy	405	RGS 407	
Db	414	RKS 416	
RESULT 11			
Db	Q96LA5	PRELIMINARY; PRT; 508 AA.	
Qy	AC Q96LA5;		
Db	DT 01-DEC-2001 (TREMBLrel. 19, Created)		
Qy	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
Db	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
Qy	DE FC receptor-like protein 2 (FcRH2).		
Db	GN Name=FCRH2; ORFNames=UNQ9236;		
Qy	OS Homo sapiens (Human).		
Db	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Qy	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Db	OX NCBI_TaxID=9606;		
Qy	RN [1]		
Db	RP SEQUENCE FROM N.A.		
Qy	RP MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;		
Db	RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
Qy	RT "Identification of a family of Fc receptor homologs with preferential		
Db	RT B cell expression.";		
Qy	RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).		
Db	RN [2]		
Qy	RP SEQUENCE FROM N.A.		
Db	RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
Qy	RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
Db	RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
Qy	RA Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
Db	RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
Qy	RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
Db	RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
Qy	RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
Db	RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
Qy	RA Godowski P.;		
Db	RT "The secreted protein discovery initiative (SPDI), a large-scale		
Qy	RT effort to identify novel human secreted and transmembrane proteins: a		
Db	RT bioinformatics assessment.";		
Qy	RL Genome Res. 13:2265-2270 (2003).		
Db	DR EMBL; AV043465; AAK91778.1; -		
Qy	DR EMBL; AV358130; AAK88497.1; -		
Db	DR HSP; P12319; IF2Q.		
Qy	DR HSP; HGNC:14875; SPAP1.		
Db	DR GO; GO:0004872; Fc receptor activity; IEA.		
Qy	DR InterPro; IPR007110; Ig-like.		
Db	DR Pfam; PF00047; Ig; 3.		
Qy	DR PROSITE; PS50835; IG_LIKE; 3.		
Db	KW Receptor.		
Qy	SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;		

Db	1	MLLWASLLAFAPVCCQSAAHKPVLSVHPPTTFKGERVTLTCNGQFYATEKTTWYHR	60
Qy	61	YLKGEKLTITPGNTLEVRSGLYRCQARGSPRNPVRLTFSSDSLLOAPYSVFEGLTV	120
Db	61	HTWGEKLTITPGNTLEVRSGLYRCQARGSPRNPVRLTFSSDSLLOAPYSVFEGLTV	120
Qy	121	LRCKRAEAVTLNNTYK-NDNVIAFLNKRTPHACLKONGAYRCTGYKESCCPVSSN	179
Db	121	LRCHRRRKEKLTAVKYTWNGNLTLSNKSVDLLIPQASNNNGNRCICYGENDVFRSN	180
Qy	180	TVKIQVOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVLPFRFFRDDQTLGLGW	239
Db	181	FKIIKIQELFPPHPELKATDSQTEGNSVNLSCETQLPPERSDTPLFHFNFRDGEVILSDW	240
Qy	240	SLSNPFQITAMWSKSGFYWCXAAATPHSVISDSPRSWIQV-IPASHPVLTLSPKALN	298
Db	241	STYPELQLPTVWRENSGSYWCAGETVRGNIHKHSPSLQIHVORI	300
Qy	299	FEKTKVTLHCEETOEDSLRTLYRPFYHEGV-PLRHKSVCRCERGASISFSLTTENSNNYCT	356
Db	301	VEGEMLVLCVSAEGTDTFFSHREDMQESLGRKTQSLRAELELPAIROSHAGGYCT	360
Qy	357	ADNGLGAKPSKAVSLSVTVFVSHPVNLSPEDLIFEQA-----KVTLLHCEAQ	404
Db	361	ADNSYG--PVQSMVNLVTVRETP-----GNRDGLVAAGATGGLLSALLLAVALLFHCWRR	413
Qy	405	RGS 407	
Db	414	RKS 416	
RESULT 10			
Db	Q96RE0	PRELIMINARY; PRT; 515 AA.	
Qy	AC Q96RE0;		
Db	DT 01-DEC-2001 (TREMBLrel. 19, Created)		
Qy	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
Db	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
Qy	DE FC receptor-like protein 4.		
Db	GN Name=FCRH4;		
Qy	OS Homo sapiens (Human).		
Db	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Qy	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Db	OX NCBI_TaxID=9606;		
Qy	RN [1]		
Db	RP SEQUENCE FROM N.A.		
Qy	RP MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;		
Db	RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
Qy	RT "Identification of a family of Fc receptor homologs with preferential		
Db	RT B cell expression.";		
Qy	RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).		
Db	DR EMBL; AF397452; AAK93970.1; -		
Qy	DR HSP; P12319; IF2Q.		
Db	DR GO; GO:0004872; Fc receptor activity; IEA.		
Qy	DR InterPro; IPR003598; IG_C2.		
Db	DR SMART; SM00408; IGC2; 1.		
Qy	DR PROSITE; PS50835; IG_LIKE; 4.		
Db	KW Receptor.		
Qy	SQ SEQUENCE 515 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;		
Query Match			
Best Local Similarity 43.3%; Pred. No. 8.9e-51;			
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;			
Qy	1	MLLWASLLAFAPVCCQSAAHKPVLSVHPPTTFKGERVTLTCNGQFYATEKTTWYHR	60
Db	1	MLLWASLLAFAPVCCQSAAHKPVLSVHPPTTFKGERVTLTCNGQFYATEKTTWYHR	60
Qy	61	YLKGEKLTITPGNTLEVRSGLYRCQARGSPRNPVRLTFSSDSLLOAPYSVFEGLTV	120

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Query Match      24.8%; Score 773.5; DB 2; Length 508;
Best Local Similarity 47.3%; Pred. No. 2.1e-47;
Matches 178; Conservative 46; Mismatches 137; Indels 15; Gaps 6;

QY 104 SLIIQAPLSVFEQDSVVLRCRAKAEVTLNNTIYKNDN-VLAFLNKRTPDHPHACLKNDG 162
DB 19 SLTLVAFSSVFEQDSIVLKQGEQNWIKQMAVHKDKNELSVFKFSDFLIQSAVLSDSG 78

QY 163 AYRC-TGYKSCCPVSSNTVKIQVQEPFTRPVLRASSFQPIISGNPVTLCETQLSLERSD 221
DB 79 NYFCSTKGQLFLWDKTSNIVKIKVQELQRPVLTASSFQPIEGGPVSLKCETRLSPQRLD 138

QY 222 VPLRFRFRDDQTLGLGWSLSPNQITAMSKDSGFWYCKAATMHPHVSIDSRSRSTQVQ 281
DB 139 VQLQFCFRENQVLGWSWSSPELQISAVWSEDTGYSWYCAETVTHRIKQSLQSHVQ 198

QY 282 -IPASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTYRPFYH--GVPLRHKSVCRCRG 338
DB 199 RPIPSNVSLRAGPGQGVQTEGQKLILCSVAGGNGVTFSTYREATGSMGKKTQR---- 254

QY 339 ASISFSL-----TTENSGNYCTADNGLGAKPKSKAVSLSTVPVSHPVNLSPEDLIPE 393
DB 255 -SLSAELEIPAVKESDAGKYCRADNGHVPIQSKVNPVPIVSRPVLTLRSPGAQAV 313

QY 394 GAKVTLHCEAQRSLPILYQFHEDAAALBRRSANSAGGVAISFSLTAHSGNYCTADNG 453
DB 314 GDLELHCEALRGSPILYQFYHEDVTLGNSSAPSGGGSFNLSTLAHSGNSYCEANNG 373

QY 454 FGQRSKAVSLSTVP 469
DB 374 LGAQCSEAVPVSISGP 389

RESULT 12
Q8N732 PRELIMINARY; PRT; 360 AA.
AC Q8N732;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE DJ80IG22.1 (Novel immunoglobulin domain protein similar to
DE immunoglobulin receptors) (fragment).
GN Name=dj80IG22.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL13529; CAB92753.1; -.
DR HSP; P12319; I2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
KW RECEPTOR.
FT NON_TER 1
FT NON_TER 360
SQ SEQUENCE 360 AA; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match      24.7%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred. No. 1.7e-47;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIIFLPQPTVTFQGERVLTCKGRRFFYSQTKVHYRLGKILLRETPDNILEVQESG 81
DB 4 KPVISVHPPTTFFKGERVLTLCNGFQFYATEKNTVHRRHWGKELTLTPGNTLVRESG 63

82 EYRCQAGSPLSSPVHLDPFSSASLILOAPLSVFEQDSVVLRCRAKAEVTLNNTIYK-NDN 140
DB 64 LYRCQAGSPLSSPVHLDPFSSASLILOAPLSVFEQDVLVLRCHRRREKLTAVKYTWNGN 123

QY 141 VLAFLNKRTPDHPHACLKNDGAYRCCTGYKSCCPVSSNTVKIQVQEPFTRPVLRASSFQ 200
DB 124 ILSISNKSWDLLIPQASSNNNGNYRCIGYDENDVFRSNPKIKIQELFPHPELKATDSQ 183

QY 201 PISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWSLSPNQITAMSKDSGFWYCW 260
DB 184 PTEGNSVNLSCETQLPERSDTPLFHNFRRFDGEVILSDWSTYPELQPLTWRENSGSWYC 243

QY 261 KAMTMSHVSIDSRSRSTQVQ-IPASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTY 319
DB 244 GAETVRGNIHKHSPSLQIHVQRIPVSGVILLETQPSGGQAVEGEMLVLCVSAEGTGDTTF 303

QY 320 RFYHEGV--PLRHKSVCRCGASISFSLTTENSGNYCTADNGLGAKPKSKAVSLSTVP 375
DB 304 SWHREDQBSLGRKTRSLRAELPAIROSHAGGYCTADNSYG--PVQSMVLNVTV 359

RESULT 13
Q8BJA5 PRELIMINARY; PRT; 508 AA.
AC Q8BJA5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
DE library, clone: F830015f10 product: weakly similar to SH2 DOMAIN-
DE CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaehizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaehizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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Thu May 5 15:10:59 2005

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [16]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089756; BAC40954.1; -.
DR HSP; P12319; IP2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR SEQUENCE 508 AA; 56795 MW; 27774A4733A9443F CRC64;
SQ
Query Match 22.2%; Score 692.5; DB 2; Length 508;
Best Local Similarity 40.9%; Pred. No. 1.5e-41;
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;
QY 105 LILQAPLSVFGDSVLRCAAEVTLNN-TYKNDNVLAFLNKRDFPHACLKDNKA 163
DB 31 LVLOAPPVAFEGDSVLRCAAEVTLNN-TYKNDNVLAFLNKRDFPHACLKDNKA 90
QY 164 YRCTGYKESC--CRVSNTVKIQVEPTFPLVRASQFIPISGNPTLCETQLSERSD 221
DB 91 YKCTSKKWSFGSLYTSNTVRVQVELFPRPVLRAKPSHPIDGSPVLTCTQLSAQSD 150
QY 222 VPLRFRPRDQTLGLHSLSPNFOITAMWSKDSGFYKCAATWPHSVISDSRSTQVQ 281
DB 151 ARLOPFCFRNLQLLGSGCSRSSEFHPAIVTEESKRYOQKAETVNSQVRKQSTAFIPVQ 210
QY 282 IPASHPVLTLPGERKALNFEKTKVTLHCETQEDSLRTLYRFYHEGVP-----LRH 330
DB 211 RASARFQTHIPASKLVFEGQLLLNCSV-----KGVPGPKFWSYKMDLN 257
QY 331 KSVRCERGASISFSLTTN-----SGNYCTADNGLGAKPSKAVLSVTPVPSHPVLNLSPP 387
DB 258 KETKILKSNABFKISQVNIADAGYHREATNRRSFVSRAPFIIKVPVQSVPLTSTG 317
QY 388 EDLIEGAKVTLHCERQSGSLPILYQFPHHDAALERRSANSAGGVAFISFSLTAHSGNY 447
DB 318 KTOALEGDLMTLHCOSQSGPCLLYEYFENVSLGNSILSGGAYFNFSMSTERSGNY 377
QY 448 CTADNGFGPQRSKAVLSL-----TVPVS 471
DB 378 CTADNGLGACQCEAARISIFDMTKNRSVFMA 408
RESULT 14
Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Name=FLJ00333;

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR NON_TER 1
FT SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;
SQ
Query Match 21.0%; Score 657.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.2e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;
QY 291 LSPKALNFEKTK-----VTLHCETQEDSLRTLYRFYHEGVPPLRHKSVCERGSISFS 344
DB 24 LAPSPSGGFPQAQVVDLLEHCEAPRGSPPLLYFYHEDVTLGSSSAPSGGCEASFNL 83
QY 345 LTTNSNGNYCTADNGLGAKPSKAVLSVTPVPSHPVLNLSPPEDLIFEGAKVTLHCERQ 404
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVTPVPSRPLTPRAPRAQAVVDLLEHCEAL 143
QY 405 RGSPLILYQFPHHDAALERRSANSAGGVAFISFSLTAHSGNYSCTADNGLGAKPSKAVSL 464
DB 144 RGSPLILYFYHEDVTLGKISAPSGGASFNLSLTTTEHSGIYSCDANGLEAQRSEWVTL 203
QY 465 SITVPVPSHPVLTLSSAEALTFEGATVTLHCERQSGSLPILYQFPHHDAALERRSANS 524
DB 204 KAVPVPSPVLTLPAPGTHAAVGLLEHCEALRGLSPILYRFYHEDVTLGNSRSPS-GG 262
QY 525 VSFPSLTFEGHSGNYSCTADNGLGAKPSKAVLSVTPVPSHPVLNLSPPEDLIFEGAKV 561
DB 263 ASLNLSLTAHSGNYSCEADNGLGAQRSEVTLVITG 299
RESULT 15
Q9EQY5 PRELIMINARY; PRT; 509 AA.
AC Q9EQY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MMAN-g protein precursor (IPGP2) (Mus musculus adult male diencephalon
DE cDNA, RIKEN full-length enriched library, clone:9330158F12
DE product:macrophage scavenger receptor 2, full insert sequence) (Mus
DE musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810439C17 product:macrophage scavenger
DE receptor 2, full insert sequence).
DE Name=Msr2; Synonyms=MMAN-g;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA Yoshimoto M., Matsumoto K., Ukai Y., Kitamura K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guselnikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Tarantin A.V.;
RA "A family of highly diverse human and mouse genes structurally links
RT leukocyte FcR, gp42 and PECAM-1.";
RT

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Immunogenetics 54:87-95(2002).

[3] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;

RP MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX Carninci P., Hayashizaki Y.;

RA "High-efficiency full-length cDNA cloning.";

RT Meth. Enzymol. 303:19-44(1999).

[4] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;

RP MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX RIKEN FANTOM Consortium;

RA "Functional annotation of a full-length mouse cDNA collection.";

RT Nature 409:685-690(2001).

[5] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;

RP The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RX Nature 420:563-573(2002).

[6] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;

RP MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RX Genome Res. 10:1617-1630(2000).

[7] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;

RP MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RX Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RX Genome Res. 10:1757-1771(2000).

[8] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Diencephalon;

RP Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kogawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[9] SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Whole body;

RP Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,

RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB028174; BAB18569.1; -

DR EMBL; AF329486; AAL23896.1; -

DR EMBL; AK034125; BAC28595.1; -

DR EMBL; AK076123; BAC36201.1; -

DR HSP; Q08380; IBY2.

DR MGD; MGI:1933397; Msr2.

DR GO; GO:0005615; C:extracellular space; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig\_c2.

DR InterPro; IPR001190; Srcr\_receptor.

DR Pfam; PF00047; Ig; 3.

DR Pfam; PF00530; SRCR; 1.

DR PRINTS; PR00258; SPERACTRCPTR.

DR SMART; SM00408; IGC2; 2.

DR SMART; SM00202; SR; 1.

DR PROSITE; PSS00835; IG\_LIKE; 4.

DR PROSITE; PS00420; SRCR\_1; 1.

DR PROSITE; PS00287; SRCR\_2; 1.

KW Receptor; Signal.

FT SIGNAL 1 17 Potential.

FT CHAIN 18 509 Potential.

SQ SEQUENCE 509 AA; 55787 MW; EAB422EAC1310ECC CRC64;

Query Match 19.2%; Score 600.5; DB 2; Length 509;

Best Local Similarity 30.4%; Pred. No. 6.6e-35;

Matches 147; Conservative 71; Mismatches 159; Indels 107; Gaps 8;

Qy 96 VHLDFSSAIILOAPLSVFEGDSVLRCAKAEVLTNNTYKQDNV-LAFLNKRTDHPH 154

Db 15 VQSDWLSISL-----PHRSYEGDQVWISCTGNNGDIKRLKYFKDGYHIETSSASYTIR 70

Qy 155 HACLKONGAYRCTGYKESCCPV-----SSNTVKIQVQEPFTRPVLRASSFQISGNPVTIT 210

Db 71 NARGDSGSGYCKADRRKFFLIDTTEGTGKWLNVQELFPAPGLTASPLQFVEGSSVTLS 130

Qy 211 CETQLSLERSDVLPRFRFRDQDTGLGWSLSPNFQITAMWSKDSGFYWCKAATMPSVI 270

Db 131 CNTWLPDSRATTQLRYSFFKDGHTLQSGWT-SSKFTLSISKEDSGNYWCMTASRSVS 189

Qy 271 SDSPRSWIQVQ-IPASHPVLTLSPEKALNPEGTQVTLHCETQEDSLRTLYFYHEGVPLR 329

Db 190 KQSHRSYIDVERIPVSQVMTMEIQPSRGWVEG----- 221

Qy 330 HKSVRCERGASISFSLTTEGSGNYCYCTADNGLGAKPSKAVSLVTPVPSHPVLNLSPPED 389

Db 222 -----EP 223

Qy 390 LIPEGAKVTLHCEAQRGSLPILYQFTHEDA--ALERRSANSAGGVAISFSLTASHSGNY 447

Db 224 LVVEGEPVLVACSVAKGTGLITFSWRODTKESVGKKSQRVSQORVELEIPITRESHAGYY 283

Qy 448 CTADNCGFGPQRSKAVSLITVPSVHPVLTLSABALTFEGATVTLHCEVQRGSPQILYQF 507

Db 284 CTADNNYGLIQSAIVNITVKIPVLNPLLSISVPGVLPFFIGDVAELHCEDKRASPPVLYWF 343

Qy 508 YHEDMPLVSSSTPSVGRVSFSLTEGHSNGNYCYCTADNCGEPQSRSEVVSFLVTCCKWILA 567

Db 344 YHENITLANTSAPFGKASFKLSLTAGHSNGNYCYCTADNCGEPQSRSEVVSFLVTCCKWILA 567

Qy 568 SKPP 571

Db 397 -EPP 399

Search completed: May 4, 2005, 11:38:00

Job time : 82.8488 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 125.902 Seconds  
(without alignments)  
3001.261 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 5116

Sequence: 1 MLWVILLVLPVSGQFART.....KVASTPVSGSLFIASSAPHR 977

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5116	100.0	977	4	AAB82315 Human imm
2	5116	100.0	977	7	ADM35237 Human LY1
3	5104	99.8	977	6	ABP97215 Tumour-as
4	4486	87.7	875	8	ABM82476 Human dia
5	4253	83.1	837	8	ABM82477 Human dia
6	3923	76.7	759	4	AAB82313 Human imm
7	3923	76.7	759	7	ADM35235 Human LY1
8	2962	57.9	592	4	AAB82314 Human imm
9	2962	57.9	592	7	ADM35236 Human LY1
10	1559	30.5	707	7	ADM06089 Human pro
11	1559	30.5	734	4	AAB82316 Human imm
12	1559	30.5	734	7	ADM35238 Human LY1
13	1556.5	30.4	733	8	ADL06557 Human tum
14	1541.5	30.1	727	6	ABB84668 Human SEC
15	1538.5	30.1	750	8	ABM84916 Human dia
16	1520	29.7	717	7	ADF74337 Human FCR
17	1516	29.6	717	7	ADF74338 Human FCR
18	1411	27.6	582	6	ABU99155 Novel hum
19	1411	27.6	582	8	ADM33875 Human NOV
20	1408.5	27.5	718	8	ABM84917 Human dia
21	1376	26.9	707	8	ABM84918 Human dia
22	1367.5	26.7	554	7	ADF74336 Extracell
23	1205.5	23.6	639	7	ADJ70604 Human hea
24	1185	23.2	655	8	ABM84920 Human dia
25	1137	22.2	268	7	ADE08350 Novel pro

26	1120	21.9	222	5	ABP69283 Human pol
27	1116.5	21.8	641	8	ABM84919 Human dia
28	1029	20.1	570	7	ADF74389 Murine FC
29	1024.5	20.0	470	7	ADL22727 Human dis
30	931.5	18.2	508	4	AAB82317 Human imm
31	931.5	18.2	508	7	ADM35239 Human LY1
32	931.5	18.2	508	7	ADM35264 Human LY1
33	931.5	18.2	508	8	ADF89715 Human can
34	931.5	18.2	508	8	ADL06539 Human tum
35	927.5	18.1	489	7	ADF74316 Human FCR
36	900	17.6	181	5	ABP51264 Human MDD
37	900	17.6	181	5	ABP51409 Human MDD
38	889	17.4	468	7	ADF74391 Extracell
39	884.5	17.3	327	5	ABP63021 Human pol
40	871.5	17.0	421	6	ABU99156 Novel hum
41	871.5	17.0	421	6	ABU99157 Novel hum
42	871.5	17.0	421	8	ADM93877 Human NOV
43	864.5	16.9	445	7	ADM35268 Human LY1
44	861	16.8	460	7	ADM35273 Human LY1
45	858.5	16.8	380	7	ADF74334 Extracell

ALIGNMENTS

RESULT 1

AAB82315

ID AAB82315 standard; protein; 977 AA.

XX AC AAB82315;

DT 23-JUL-2001 (first entry)

XX Human immunoglobulin receptor isoform IRTA2c.

DE Immunoglobulin superfamily receptor translocation associated; IRTA;

KW IRTA2c; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;  
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..15
Protein	/label= Signal_peptide
Modified-site	16..977
Modified-site	/label= Mature_protein
Modified-site	132..134
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	383..385
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	621..623
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	631..633
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	714..716
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	795..797
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	806..808
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	816..818
Modified-site	/note= "Asn is N-glycosylated"
Modified-site	843..845
Modified-site	/note= "Asn is N-glycosylated"
Domain	851..873
Binding-site	/note= "transmembrane domain"
Binding-site	899..902
Binding-site	/note= "putative consensus Src-homology 2 (SH2) binding domain"
Binding-site	924..927
Binding-site	/note= "putative consensus Src-homology 2 (SH2) binding domain"
Binding-site	954..957

Thu May 5 15:11:00 2005

/note= "putative consensus Src-homology 2 (SH2) binding domain"

WO200138490-A2.

31-MAY-2001.

28-NOV-2000; 2000WO-US032403.

29-NOV-1999; 99US-0168151P.

(UYCO ) UNIV COLUMBIA NEW YORK.

Dalla-Favera R;

WPI; 2001-355921/37.

N-PSDB; AAF30952.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2c (IRTA2c), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314). IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein. Each SH2 binding site agrees with the immune receptor tyrosine-based inhibition motif (ITIM) consensus and is encoded by a separate exon. The IRTA2 genes display a specific pattern of expression in mature B cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to epitopes of IRTA proteins. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridizes with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridizes to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 977 AA;

Query Match 100.0%; Score 5116; DB 4; Length 977;  
Best Local Similarity 100.0%; Pred. No. 2.le-315;  
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPPWTVFGGERVLTCKGFRFYSPQKTWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLPQPPWTVFGGERVLTCKGFRFYSPQKTWYHR 60  
QY 61 YLQKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSALILQAPLSVFEGDSV 120  
DB 61 YLQKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSALILQAPLSVFEGDSV 120  
QY 121 LRCRAKEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTGKSCCPVSNT 180  
DB 121 LRCRAKEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTGKSCCPVSNT 180  
QY 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCEITQSLERSDVLPRFRFRDDQTLGLWS 240

DB 181 VKIQVQEPFTRPVLRASSFQPSIGNPVTLTCEITQSLERSDVLPRFRFRDDQTLGLWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSHIOVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSHIOVQIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETQDSLTLYRFYHGVPLRHKSVCERCASISFSLTTTNSGNYCYCTADNG 360  
DB 301 GTKVTLHCETQDSLTLYRFYHGVPLRHKSVCERCASISFSLTTTNSGNYCYCTADNG 360  
QY 361 LGAKPSKAVSLSVTVVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPIYQPHHEDA 420  
DB 361 LGAKPSKAVSLSVTVVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPIYQPHHEDA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTVVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTVVSHPVLTLSA 480  
QY 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSGRVSFSLTEGHSNYY 540  
DB 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSGRVSFSLTEGHSNYY 540  
QY 541 CTADNGFGPQPSVSLFVTVVSRPILTLRVPRQAQVVDLLELHCEAPRGPSPILYWF 600  
DB 541 CTADNGFGPQPSVSLFVTVVSRPILTLRVPRQAQVVDLLELHCEAPRGPSPILYWF 600  
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660  
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660  
QY 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGASFNLSLTTT 720  
DB 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGASFNLSLTTT 720  
QY 721 HSGYSCADNGLERQSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLELHCEALRGSP 780  
DB 721 HSGYSCADNGLERQSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLELHCEALRGSP 780  
QY 781 LILYRFHEDVTLGNRSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVLYITGL 840  
DB 781 LILYRFHEDVTLGNRSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVLYITGL 840  
QY 841 TANRSGPATVAGGLLSIAGLAAAGALLYCWLSRKAGRKPADPARSPSDSDSQEPTYH 900  
DB 841 TANRSGPATVAGGLLSIAGLAAAGALLYCWLSRKAGRKPADPARSPSDSDSQEPTYH 900  
QY 901 NYPAMEELQPVVYTNANPRGENVYSEVRIOEKKHVAASDPRLRNKGSPIIYSEKVA 960  
DB 901 NYPAMEELQPVVYTNANPRGENVYSEVRIOEKKHVAASDPRLRNKGSPIIYSEKVA 960  
QY 961 STPVSGSLFLASSAPHR 977  
DB 961 STPVSGSLFLASSAPHR 977

RESULT 2  
ADM35237  
ID . ADM35237 standard; protein; 977 AA.  
XX  
AC ADM35237;  
XX  
DT 03-JUN-2004 (first entry)  
XX Human LY1448P cancer related protein for cancer detection method.  
XX Cytostatic; T-cell vaccine; detection; cancer;  
XX chronic lymphocytic leukemia.  
XX Homo sapiens.  
XX WO2003077836-A2.  
XX 25-SEP-2003.  
PD

XX 06-NOV-2002; 2002WO-US035728.  
XX 06-NOV-2001; 2001US-00040862.  
XX 23-NOV-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.  
XX Gaiger A, Algate PA, Mannion J, Retter M;  
XX WPI; 2003-756941/71.  
XX Detecting cancer in a patient comprises contacting a biological sample  
XX from the patient with a binding agent that binds to a cancer-associated  
XX polypeptide and comparing the amount of polypeptide to a predetermined  
XX cutoff value.  
XX Disclosure; SEQ ID NO 10462; 419pp; English.  
XX The invention relates to a method of detecting (M1) cancer in a patient  
XX by: (i) contacting a biological sample from the patient with an agent  
XX that binds to any of three polypeptides given in the specification; (ii)  
XX detecting in a sample an amount of the peptide that binds to the binding  
XX agent; and (iii) comparing the amount of polypeptide present in the  
XX patient's sample to a predetermined cutoff value. The specification also  
XX discloses a separate method for detecting (M2) cancer in a patient by a  
XX method similar to M1, except that the detection agent is an  
XX oligonucleotide that binds to any of three polynucleotides given in the  
XX specification. M1 and M2 are useful for detecting the presence of cancer  
XX in a patient, especially chronic lymphocytic leukemia. The applicants  
XX have identified specific human polypeptides overexpressed in one or more  
XX types of hematological malignancies. This sequence corresponds to a  
XX protein used in the method of the invention.  
XX Sequence 977 AA;  
Query Match 100.0%; Score 5116; DB 7; Length 977;  
Best Local Similarity 100.0%; Pred. NO. 2.1e-315;  
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPWTTFQGERVLTCKGFRFYSPOKTKWYHR 60  
DB 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPWTTFQGERVLTCKGFRFYSPOKTKWYHR 60  
QY 61 YLCKEILRETPDNIIVQESGEYRCQAQGSPLSPVHLDPFSSASLILQAPLSVFEGDSVV 120  
DB 61 YLCKEILRETPDNIIVQESGEYRCQAQGSPLSPVHLDPFSSASLILQAPLSVFEGDSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQOEPFTRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRPDQDTLGLWS 240  
DB 181 VKIQOEPFTRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRPDQDTLGLWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETOBSLRTLRYFYHEGVPLRHKSVCRCERGASISPSLTENSNGNYCTADNG 360  
DB 301 GTKVTLHCETOBSLRTLRYFYHEGVPLRHKSVCRCERGASISPSLTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLTVPVSHVPLNLSPEDLIFGAKVTLHCEAQRSLPILYOFHEDAA 420  
DB 361 LGAKPSKAVSLTVPVSHVPLNLSPEDLIFGAKVTLHCEAQRSLPILYOFHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPVSHVPLTSSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPVSHVPLTSSA 480  
QY 481 EALTFFEGATVTLHCEVQGRSPQILYQFYHEDMPLWSSTPSVGRVSFSLTEGHSNGNY 540

DB 481 EALTFFEGATVTLHCEVQGRSPQILYQFYHEDMPLWSSTPSVGRVSFSLTEGHSNGNY 540  
QY 541 CTADNGFGPQRSVWSLFTVTPVSRPILTLRVPRAAVVGDLLELHCEAPRGSPPILYWF 600  
DB 541 CTADNGFGPORSVWSLFTVTPVSRPILTLRVPRAAVVGDLLELHCEAPRGSPPILYWF 600  
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVQAHSDTISLSVIVPVSRI 660  
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANNGLVQAHSDTISLSVIVPVSRI 660  
QY 661 LTFRAQAQAVGVDLLELHCEALRGSPPILYWYHEDVTLGKISAPSGGASFNLSLTTE 720  
DB 661 LTFRAQAQAVGVDLLELHCEALRGSPPILYWYHEDVTLGKISAPSGGASFNLSLTTE 720  
QY 721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780  
DB 721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780  
QY 781 LILYRFFHEDVTLGNRSSPSGGASLNLSTAHSNGNYSCEADNGLGAQRSETVLYITGL 840  
DB 781 LILYRFFHEDVTLGNRSSPSGGASLNLSTAHSNGNYSCEADNGLGAQRSETVLYITGL 840  
QY 841 TANRSPPFATGAGGILLSTAGLAAGALLLYCWLRSKAGRKPAADPARSPSDSDSQEPTYH 900  
DB 841 TANRSPPFATGAGGILLSTAGLAAGALLLYCWLRSKAGRKPAADPARSPSDSDSQEPTYH 900  
QY 901 NVPAAWELOPVYTNANPRGENVYSEVRIIOEKKHAVASDRHLRNKSGSPIIYSEVKVA 960  
DB 901 NVPAAWELOPVYTNANPRGENVYSEVRIIOEKKHAVASDRHLRNKSGSPIIYSEVKVA 960  
QY 961 STPVSGSLFLASSAPHR 977  
DB 961 STPVSGSLFLASSAPHR 977  
RESULT 3  
ABP97215  
ID ABP97215 standard; protein; 977 AA.  
XX  
AC ABP97215;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Tumour-associated antigenic target protein TAT374 SEQ ID NO:97.  
XX  
KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;  
KW cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2003024392-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 11-SEP-2002; 2002WO-US028859.  
XX  
PR 18-SEP-2001; 2001US-0323268P.  
XX  
PR 19-OCT-2001; 2001US-0339227P.  
XX  
PR 07-NOV-2001; 2001US-0336827P.  
XX  
PR 20-NOV-2001; 2001US-0331906P.  
XX  
PR 02-JAN-2002; 2002US-034544P.  
XX  
PR 03-APR-2002; 2002US-0369724P.  
XX  
PR 19-AUG-2002; 2002US-0404809P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;  
XX Williams PM, Wu TD, Zhang Z;  
XX  
XX WPI; 2003-354551/33.  
XX  
XX N-PSDB; ACC49533.  
XX

Qy	1	MLLWILLIVLAPVSGOFARTPRPILFILOPWTWTFQGERVTLTCKGFRYSPOKTKWYHR	60
Db	1	MLLWILLIVLAPVSGOFARTPRPILFILOPWTWTFQGERVTLTCKGFRYSPOKTKWYHR	60
Qy	61	YLKGEILRETNDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSV	120
Db	61	YLKGEILRETNDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSV	120
Qy	121	LRCRAKAEVTLNNTIYKXNDVLAFLNKRTOPIPHACLKONGAYRCTGYKESCCPVSSNT	180
Db	121	LRCRAKAEVTLNNTIYKXNDVLAFLNKRTOPIPHACLKONGAYRCTGYKESCCPVSSNT	180
Qy	181	VKIQVEPPTRPVLRASSFQPISGNPVTLTCTQTSLERSDVPRLFRFRDDQOTGLGWS	240
Db	181	VKIQVEPPTRPVLRASSFQPISGNPVTLTCTQTSLERSDVPRLFRFRDDQOTGLGWS	240
Qy	241	LGSNFOITAMWKSODSGFWCKAAWPHSVISDSPRSWIQVQIPASHPVLTLSEKALNEE	300
Db	241	LGSNFOITAMWKSODSGFWCKAAWPHSVISDSPRSWIQVQIPASHPVLTLSEKALNEE	300
Qy	301	GTKVTLHCETQSDSLRTLRYRFVHEGVPLRHKSVCERCASISFSLATTENSGNYICTADNG	360
Db	301	GTKVTLHCETQSDSLRTLRYRFVHEGVPLRHKSVCERCASISFSLATTENSGNYICTADNG	360
Qy	361	LGAKPSKAVSLSVTPVSPHVLNLISSPDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA	420
Db	361	LGAKPSKAVSLSVTPVSPHVLNLISSPDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA	420
Qy	421	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGCPQRSKAVSLIITVPVSHPVLTLSSA	480
Db	421	LERRSANSAGGVAISFSLTAEHSGNYYCTADNGCPQRSKAVSLIITVPVSHPVLTLSSA	480
Qy	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSPSLTEGHSNYY	540
Db	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSPSLTEGHSNYY	540
Qy	541	CTADNGFGPORSVWSLFTVTPVSPRILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF	600
Db	541	CTADNGFGPORSVWSLFTVTPVSPRILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF	600
Qy	601	YHEDVTLTGSSSPAGSGEASFNLSTAHSNGNYSCEANNGLVAQHSDTISLSVIPVSRPI	660
Db	601	YHEDVTLTGSSSPAGSGEASFNLSTAHSNGNYSCEANNGLVAQHSDTISLSVIPVSRPI	660
Qy	661	LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTILGKISAPSGGASFNLSLTTE	720
Db	661	LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTILGKISAPSGGASFNLSLTTE	720

QY	721	HSGIYCEADNGLEAQRSENVTLKVAVPVSRPVLTLRAPOTHAAGVDLLLEHCEALRGSP	780
DB	721	HSGIYCEADNGPEAQRSENVTLKVAVPVSRPVLTLRAPOTHAAGVDLLLEHCEALRGSP	780
QY	781	LIILYRFHEDVTIGNRSSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVLYITGL	840
DB	781	LIILYRFHEDVTIGNRSSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVLYITGL	840
QY	841	TANRSGPPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPASDPARSPDSDSQEPYTH	900
DB	841	TANRSGPPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRKPASDPARSPDSDSQEPYTH	900
QY	901	NVPAAWELOQVYTNANPRGENVYSEVRITIOEKKKHAVASDPHRLRNKGSPIIYSEVKVA	960
DB	901	NVPAAWELOQVYTNANPRGENVYSEVRITIOEKKKHAVASDPHRLRNKGSPIIYSEVKVA	960
QY	961	STPVSGSLFLASSAPHR	977
DB	961	STPVSGSLFLASSAPHR	977
RESULT 4			
ABM82476			
ID	ABM82476 standard; protein; 875 AA.		
XX	AC ABM82476;		
XX	18-NOV-2004 (first entry)		
XX	Human diagnostic and therapeutic pprotein SEQ ID NO:2725.		
XX	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.		
XX	Homo sapiens.		
OS	WO2004023973-A2.		
XX	25-MAR-2004.		
XX	12-SEP-2003; 2003WO-US028227.		
XX	12-SEP-2002; 2002US-0410259P.		
PR	12-SEP-2002; 2002US-0410260P.		
XX	(INCV-) INCYTE CORP.		
XX	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Hartschorn TA, Suchorolski WT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;		
XX	WPI; 2004-329368/30.		
DR	N-PSDB; ACN41128.		
XX	New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.		
XX	Claim 27; Page; 190pp; English.		
XX	The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or		

CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 875 AA;

Query Match 87.78; Score 4486; DB 8; Length 875;  
Best Local Similarity 88.83; Pred. No. 1.6e-275;  
Matches 868; Conservative 4; Mismatches 2; Indels 104; Gaps 2;

Qy 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTWYHR 60  
Db 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTWYHR 60  
Qy 61 YLGEILRETPDNILEVOESGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
Db 61 YLGEILRETPDNILEVOESGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240  
Qy 241 LSPNQITAMWSKDSGYWCKAATMPSHVSIDSPRSIVQIOPASHPVLTLSPKALNPE 300  
Db 241 LSPNQITAMWSKDSGYWCKAATMPSHVSIDSPRSIVQIOPASHPVLTLSPKALNPE 300  
Qy 301 GTKVTLCETQDSRLTYFYHEGVPLRHKSVRCERGASISLTTENGNYCYTADNG 360  
Db 301 GTKVTLCETQDSRLTYFYHEGVPLRHKSVRCERGASISLTTENGNYCYTADNG 360  
Qy 361 LGAKPSKAVSLTVTPVSHVPLNLSSPEDIIFGAKVTLHCEAQRGSLPLIYQFHEDAA 420  
Db 361 LGAKPSKAVSLTVTPVSHVPLNLSSPEDIIFGAKVTLHCEAQRGSLPLIYQFHEDAA 420  
Qy 421 LERRSANSAGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSSA 480  
Db 421 LERRSANSAGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSSA 480  
Qy 481 EALTFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSTPSVGRVSFSLTGHSGNYY 540  
Db 481 EALTFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSTPSVGRVSFSLTGHSGNYY 540  
Qy 541 CTADNGFGPQRSEVSLF-VTVPSRPIILTRVPRAQAVVGDILLEHCEAPRGPPILYW 599  
Db 541 CTADNGFGPQRSEVSLFVSFVSVPSPILTRVPRAQAVVGDILLEHCEAPRGPPILYW 600  
Qy 600 FYHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRP 659  
Db 601 FYHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRP 660  
Qy 660 ILTFRAPRAQAVVGDILLEHCEALRGSSPILYFPHYHEDVTGKISAPSGGGASFNLSLT 719  
Db 661 ILTFR----- 665  
Qy 720 EHSGLYSCEADNGLEAQRSEMTLKVAVPVRPVLTLRAPGTHAAVGDILLEHCEALRG 779  
Db 666 -----LLEHCEALRG 677  
Qy 780 PLILYRFFHEDVTIGNRSSPGGASLNLSTABHSGNYSCEADNGLGAQRSEVTLIYIG 839  
Db 678 PLILYRFFHEDVTIGNRSSPGGASLNLSTABHSGNYSCEADNGLGAQRSEVTLIYIG 737  
Qy 840 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGRKPSADPARSPSDSDSQBPTY 899  
Db 840 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGRKPSADPARSPSDSDSQBPTY 899

Db 738 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGRKPSADPARSPSDSDSQBPTY 797  
Qy 900 HNPVAMEELQPVVTNANPRGENVYSEVRIIQEKKKHAVASDPRHLRNKSGPIIYSEVKV 959  
Db 798 HNPVAMEELQPVVTNANPRGENVYSEVRIIQEKKKHAVASDPRHLRNKSGPIIYSEVKV 857  
Qy 960 ASTPVSGLSFLASSAPHR 977  
Db 858 ASTPVSGLSFLASSAPHR 875

RESULT 5  
ABM82477  
ID ABM82477 standard; protein; 837 AA.  
XX  
AC ABM82477;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2726.  
XX  
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
XX  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve JL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;  
PI Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patuty S, Shi X, Suarez CJ;  
XX  
XX WPI: 2004-329368/30.  
DR N-PSDB; ACN41129.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 837 AA;

Query Match		83.1%;	Score 4253;	DB 8;	Length 837;
Best Local Similarity		84.8%;	Pred. No. 8.6e-261;		
Matches 829;		Conservative 4;	Mismatches 3;	Indels 142;	Gaps 3;
Qy	1	MLLWVLLVLPVSGQFARTPRPIIFLQPPWTTVFOGSRVTLTKGFRFYSPQTKVYHR	60		
Db	1	MLLWVLLVLPVSGQFARTPRPIIFLQPPWTTVFOGSRVTLTKGFRFYSPQTKVYHR	60		
Qy	61	YLGKILRETDPNIILEVESGEYRCQAGSPVHLDFSSASLILQAPLSVEGDSVV	120		
Db	61	YLGKILRETDPNIILEVESGEYRCQAGSPVHLDFSSASLILQAPLSVEGDSVV	120		
Qy	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRITDHI PHACLKNDGAYRCTGYKSCCPVSSNT	180		
Db	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRITDHI PHACLKNDGAYRCTGYKSCCPVSSNT	180		
Qy	181	VKIQOEPTRPVLRASSQPIISGNPVTITCETOLSLERSDVPLFRFRDDOTILGLGWS	240		
Db	181	VKIQOEPTRPVLRASSQPIISGNPVTITCETOLSLERSDVPLFRFRDDOTILGLGWS	240		
Qy	241	LSPNFOITAMWSKDSGYFKCAATPHSVISDSRWSIQVQIPASHPVLTLSPEKALNFE	300		
Db	241	LSPNFOITAMWSKDSGYFKCAATPHSVISDSRWSIQVQIPASHPVLTLSPEKALNFE	300		
Qy	301	GKVTILHCEQEDSLRTLYRFYHEGVPLRHKVRCERGASISFSLTTNSGNYCTADNG	360		
Db	301	GKVTILHCEQEDSLRTLYRFYHEGVPLRHKVRCERGASISFSLTTNSGNYCTADNG	360		
Qy	361	LGAKPSKAVSLSVTVPSHPVLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420		
Db	323	LGAKPSKAVSLSVTVPSHPVLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	382		
Qy	421	LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSVTVPSHPVLTLSSA	480		
Db	383	LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSVTVPSHPVLTLSSA	442		
Qy	481	EALTFEGATVTLCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540		
Db	443	EALTFEGATVTLCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	502		
Qy	541	CTADNGFGPQRSEVVSULF-VTVPSRPIILTRVPRAQVVGDLLELHCEAPRGSPPILYX	599		
Db	503	CTADNGFGPQRSEVVSULF-VTVPSRPIILTRVPRAQVVGDLLELHCEAPRGSPPILYX	562		
Qy	600	FYHEDVTLGSSAPSGGEAFNLSTAEHSGNYSCEANGLVAQHSNTISLVIIVPSRP	659		
Db	563	FYHEDVTLGSSAPSGGEAFNLSTAEHSGNYSCEANGLVAQHSNTISLVIIVPSRP	622		
Qy	660	ILTRAPRAQVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLTT	719		
Db	623	ILTRP-----	627		
Qy	720	EHSGIYSCEADNGLEAQRSEMVTILKVAVPVSRPVLTLRPGTHAAVGDLELHCEALRG	779		
Db	628	-----LLELHCEALRG	639		
Qy	780	PLIILYRPHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLAQRSETVTLVITG	839		
Db	640	PLIILYRPHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLAQRSETVTLVITG	699		
Qy	840	LTANRSGPFATGVAGLLSIAAGALLLYCMLSRKAGRPASDPARSFSDSDSQEPTY	899		
Db	700	LTANRSGPFATGVAGLLSIAAGALLLYCMLSRKAGRPASDPARSFSDSDSQEPTY	759		
Qy	900	HNPVWAEELQPVYTNANRGENNVYSEVR11QEKKKHVASDPHRLNKGSPILYSEVKV	959		
Db	760	HNPVWAEELQPVYTNANRGENNVYSEVR11QEKKKHVASDPHRLNKGSPILYSEVKV	819		
Qy	960	ASTPVSGLFLASSAPHR 977			
Db	820	ASTPVSGLFLASSAPHR 837			

RESULT 6	
ID	AAB82313 standard; protein; 759 AA.
XX	AC AAB82313;
XX	23-JUL-2001 (first entry)
XX	Human immunoglobulin receptor isoform IRTA2a.
XX	Immunoglobulin superfamily receptor translocation associated; IRTA;
KW	IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW	myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX	Homo sapiens.
XX	Key
FT	Peptide
FT	Protein
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
XX	WO200138490-A2.
XX	31-MAY-2001.
XX	28-NOV-2000; 2000WO-US032403.
XX	29-NOV-1999; 99US-0168151P.
XX	(UYCO ) UNIV COLUMBIA NEW YORK.
XX	Dalla-Favera R;
XX	WPI; 2001-355921/37.
XX	N-PSDB; AAF30950.
XX	New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
XX	Translocation Associated proteins, used to treat B cell malignancies
XX	including lymphomas and multiple myeloma.
XX	Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX	The present sequence is that of the novel human immunoglobulin receptor,
XX	immunoglobulin superfamily receptor translocation associated protein
XX	isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
XX	lymphoma and melanoma. Efforts to identify genes involved in chromosomal
XX	aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
XX	led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
XX	members of a novel subfamily of related receptors within the
XX	immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
XX	isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
XX	IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains
XX	followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue
XX	560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at
XX	residue 746 and extends for a further 231 residues. The IRTA genes
XX	display a specific pattern of expression in mature B cells. IRTA2 is
XX	expressed in GC centrocytes and in perifollicular cells, which may
XX	include immunoblasts and memory cells. The invention provides IRTA
XX	nucleic acids and proteins, and antibodies directed to an epitope of an
XX	IRTA protein. Methods are claimed for: detecting a B cell malignancy
XX	comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule



CC that specifically hybridizes with a unique sequence of human IRTA1-5; and  
CC treating a subject having a B cell cancer by administering an anti-IRTA  
CC antibody or an antisense oligonucleotide that specifically hybridizes to  
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.  
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
CC Hodgkin's lymphoma  
XX  
SQ Sequence 759 AA;

Query Match 76.7%; Score 3923; DB 4; Length 759;  
Best Local Similarity 100.0%; Pred. No. 6.3e-240;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLCKGFRFYSPQKTWYHR 60  
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLCKGFRFYSPQKTWYHR 60  
QY 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
DB 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTLCETQSLERSDVLPRFRDDOTLGLWS 240  
DB 181 VKIQVEPPTRPVLRASSFQPIISGNPVTLCETQSLERSDVLPRFRDDOTLGLWS 240  
QY 241 LSPNFOITAMWSKDSGYWCKAATMPSHVSISDPSRWIOVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFOITAMWSKDSGYWCKAATMPSHVSISDPSRWIOVQIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETQDSRLRTLYRHYEGVPLRHKSVCRCGASISFSLTTNSGNYCYCTADNG 360  
DB 301 GTKVTLHCETQDSRLRTLYRHYEGVPLRHKSVCRCGASISFSLTTNSGNYCYCTADNG 360  
QY 361 LGAKPSKAVSLSTVPSVSHVNLSPEDLIFGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSTVPSVSHVNLSPEDLIFGAKVTLHCEAQRGSLPILYQFHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSTVPSVSHVNLSSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSTVPSVSHVNLSSA 480  
QY 481 EALTFFGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
DB 481 EALTFFGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
QY 541 CTADNGFGPQRSVSLFVTVPSRPTLTLVRPRAQAVGDLLELHCEAPRGSPPILYWF 600  
DB 541 CTADNGFGPQRSVSLFVTVPSRPTLTLVRPRAQAVGDLLELHCEAPRGSPPILYWF 600  
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCAANGLVAQSDTISLSVIVPSRPI 660  
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCAANGLVAQSDTISLSVIVPSRPI 660  
QY 661 LTFRAPRAQAVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
DB 661 LTFRAPRAQAVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
QY 721 HSGIYSCDADNGLEAORSEMVTLKVA 746  
DB 721 HSGIYSCDADNGLEAORSEMVTLKVA 746

RESULT 7  
ADM35235  
ID ADM35235 standard; protein; 759 AA.

XX  
AC ADM35235;  
DT 03-JUN-2004 (first entry)  
DE Human LY1448P cancer related protein for cancer detection method.  
KW cytostatic; T-cell vaccine; detection; cancer;  
KW chronic lymphocytic leukemia.  
OS Homo sapiens.  
XX  
FN WO2003077836-A2.  
XX  
PD 25-SEP-2003.  
XX  
PF 06-NOV-2002; 2002WO-US035728.  
XX  
PR 06-NOV-2001; 2001US-00040862.  
PR 23-MAY-2002; 2002US-00154884.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Gaiger A, Algate PA, Mannion J, Retter M;  
XX  
DR WPI; 2003-756941/71.  
XX  
PT Detecting cancer in a patient comprises contacting a biological sample  
PT from the patient with a binding agent that binds to a cancer-associated  
PT polypeptide and comparing the amount of polypeptide to a predetermined  
PT cutoff value.  
XX  
PS Disclosure; SEQ ID NO 10460; 419pp; English.  
XX  
CC The invention relates to a method of detecting (M1) cancer in a patient  
CC by: (i) contacting a biological sample from the patient with an agent  
CC that binds to any of three polypeptides given in the specification; (ii)  
CC detecting in a sample an amount of the peptide that binds to the binding  
CC agent; and (iii) comparing the amount of polypeptide present in the  
CC patient's sample to a predetermined cutoff value. The specification also  
CC discloses a separate method for detecting (M2) cancer in a patient by a  
CC method similar to M1, except that the detection agent is an  
CC oligonucleotide that binds to any of three polynucleotides given in the  
CC specification. M1 and M2 are useful for detecting the presence of cancer  
CC in a patient, especially chronic lymphocytic leukemia. The applicants  
CC have identified specific human polypeptides overexpressed in one or more  
CC types of hematological malignancies. This sequence corresponds to a  
CC protein used in the method of the invention.  
XX  
SQ Sequence 759 AA;  
Query Match 76.7%; Score 3923; DB 7; Length 759;  
Best Local Similarity 100.0%; Pred. No. 6.3e-240; Indels 0; Gaps 0;  
Matches 746; Conservative 0; Mismatches 0;  
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLCKGFRFYSPQKTWYHR 60  
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLCKGFRFYSPQKTWYHR 60  
QY 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
DB 61 YLGEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTLCETQSLERSDVLPRFRDDOTLGLWS 240  
DB 181 VKIQVEPPTRPVLRASSFQPIISGNPVTLCETQSLERSDVLPRFRDDOTLGLWS 240  
QY 241 LSPNFOITAMWSKDSGYWCKAATMPSHVSISDPSRWIOVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFOITAMWSKDSGYWCKAATMPSHVSISDPSRWIOVQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSHVSDSPRSWIOVQIPASHVPLTSPKALNFE 300  
Qy 301 GTKVTLHCETQDSLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360  
Db 301 GTKVTLHCETQDSLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Qy 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Db 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Qy 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540  
Db 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540  
Qy 541 CTADNGFGPQRSEVSLFVTPVSPRPILTLRPVRAQAVVGDLELHCEAPRGSPILYWF 600  
Db 541 CTADNGFGPQRSEVSLFVTPVSPRPILTLRPVRAQAVVGDLELHCEAPRGSPILYWF 600  
Qy 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660  
Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660  
Qy 661 LTFPRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720  
Db 661 LTFPRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720  
Qy 721 HSGIYSCDADNGLEAQRSEWTLKVA 746  
Db 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 8

AAB82314 ID AAB82314 standard; protein; 592 AA.  
XX AC AAB82314;  
XX DT 23-JUL-2001 (first entry)  
XX DE Human immunoglobulin receptor isoform IRTA2b.  
XX KW Immunoglobulin superfamily receptor translocation associated; IRTA;  
KW IRTA2b; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;  
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..15  
FT /label= Signal\_peptide  
FT Protein 16..592  
FT /label= Mature\_protein  
FT Modified-site 132..134  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 383..385  
FT /note= "Asn is N-glycosylated"  
XX WO200138490-A2.  
XX 31-MAY-2001.  
XX 28-NOV-2000; 2000WO-US032403.  
XX 29-NOV-1999; 99US-0168151P.  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX Dalla-Favera R;  
XX

DR WPI; 2001-355921/37.  
DR N-PSDB; AAF30951.  
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor  
XX Translocation Associated proteins, used to treat B cell malignancies  
XX including lymphomas and multiple myeloma.  
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.  
XX The present sequence is that of the novel human immunoglobulin receptor,  
XX immunoglobulin superfamily receptor translocation associated protein  
XX isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of  
XX lymphoma and melanoma. Efforts to identify genes involved in chromosomal  
XX aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma  
XX led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding  
XX members of a novel subfamily of related receptors within the  
XX immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA  
XX isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).  
XX IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at  
XX residue 560, extending for a further 32 residues, whose hydrophobicity  
XX suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes  
XX display a specific pattern of expression in mature B cells. IRTA2 is  
XX expressed in GC centrocytes and in perifollicular cells, which may  
XX include immunoblasts and memory cells. The invention provides IRTA  
XX nucleic acids and proteins, and antibodies directed to an epitope of an  
XX IRTA protein. Methods are claimed for: detecting a B cell malignancy  
XX comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule  
XX that specifically hybridises with a unique sequence of human IRTA1-5; and  
XX treating a subject having a B cell cancer by administering an anti-IRTA  
XX antibody or an antisense oligonucleotide that specifically hybridises to  
XX IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
XX arrest cell growth or induce cell death of cancer cells expressing IRTA.  
XX The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
XX multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
XX large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
XX selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
XX Hodgkin's lymphoma  
XX Sequence 592 AA;

Query Match 57.9%; Score 2962; DB 4; Length 592;  
Best Local Similarity 98.6%; Pred. No. 3.8e-179;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVTFQGERVLTCTCKGFRFYSPQTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVTFQGERVLTCTCKGFRFYSPQTKWYHR 60  
Qy 61 YLGKEILRETDPNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120  
Db 61 YLGKEILRETDPNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120  
Qy 121 LRCRAKAEVTLNNTLYKNDNVLAFLNKRTDHPHACLKDNAGVACTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTLYKNDNVLAFLNKRTDHPHACLKDNAGVACTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFQPTISGNPVTCTCETQLSLERSDVPLFRFRDDQTTLGLWS 240  
Db 181 VKIQVQEPFTRPVLRASSFQPTISGNPVTCTCETQLSLERSDVPLFRFRDDQTTLGLWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSHVSDSPRSWIOVQIPASHVPLTSPKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSHVSDSPRSWIOVQIPASHVPLTSPKALNFE 300  
Qy 301 GTKVTLHCETQDSLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360  
Db 301 GTKVTLHCETQDSLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Qy 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSFSLTEHSGNYY 540  
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSFSLTEHSGNYY 540  
Qy 541 CTADNGFGPQSRSEVSLFVT----VPVSRPIL 568  
Db 541 CTADNGFGPQSRSEVSLFVTGKCWLASHPPL 572

RESULT 9  
ADM35236  
ID ADM35236 standard; protein; 592 AA.  
XX  
AC ADM35236;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
Human LY1448P cancer related protein for cancer detection method.  
XX  
cytostatic; T-cell vaccine; detection; cancer;  
XX  
chronic lymphocytic leukemia.  
XX  
Homo sapiens.  
XX  
XX  
XX W02003077836-A2.  
XX  
PD 25-SEP-2003.  
XX  
XX 06-NOV-2002; 2002W0-US035728.  
XX  
PR 06-NOV-2001; 2001US-00040862.  
PR 23-MAY-2002; 2002US-00154884.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX  
XX Gaiger A, Algate PA, Mannion J, Retter M;  
XX  
XX WPI; 2003-756941/71.  
XX  
XX  
PT Detecting cancer in a patient comprises contacting a biological sample  
PT from the patient with a binding agent that binds to a cancer-associated  
PT polypeptide and comparing the amount of polypeptide to a predetermined  
PT cutoff value.  
XX  
XX Disclosure; SEQ ID NO 10461; 419pp; English.  
XX  
CC The invention relates to a method of detecting (M1) cancer in a patient  
CC by: (i) contacting a biological sample from the patient with an agent  
CC that binds to any of three polypeptides given in the specification; (ii)  
CC detecting in a sample an amount of the peptide that binds to the binding  
CC agent; and (iii) comparing the amount of polypeptide present in the  
CC patient's sample to a predetermined cutoff value. The specification also  
CC discloses a separate method for detecting (M2) cancer in a patient by a  
CC method similar to M1, except that the detection agent is an  
CC oligonucleotide that binds to any of three polynucleotides given in the  
CC specification. M1 and M2 are useful for detecting the presence of cancer  
CC in a patient, especially chronic lymphocytic leukemia. The applicants  
CC have identified specific human polypeptides overexpressed in one or more  
CC types of hematological malignancies. This sequence corresponds to a  
CC protein used in the method of the invention.  
XX  
XX Sequence 592 AA;  
XX  
Query Match 57.9%; Score 2962; DB 7; Length 592;  
Best Local Similarity 98.6%; Pred. No. 3.8e-179;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
XX  
Qy 1 MLLWVILLVLPVSGQPARTPRPIIFLOPWTTFQGERVTLCKGPRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQPARTPRPIIFLOPWTTFQGERVTLCKGPRFYSPOKTKWYHR 60

Qy 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVEGDSVV 120  
Db 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVEGDSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKSCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKSCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Qy 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHSVRCERGASISFSLTTENSNGNYCTADNG 360  
Db 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHSVRCERGASISFSLTTENSNGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480  
Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSFSLTEHSGNYY 540  
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSFSLTEHSGNYY 540  
Qy 541 CTADNGFGPQSRSEVSLFVT----VPVSRPIL 568  
Db 541 CTADNGFGPQSRSEVSLFVTGKCWLASHPPL 572

RESULT 10  
ADM06089  
ID ADM06089 standard; protein; 707 AA.  
XX  
AC ADM06089;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein of the invention SEQ ID NO:4774.  
XX  
XX human; gene therapy; diagnostic marker; pharmaceutical.  
XX  
XX Homo sapiens.  
XX  
XX EP1347046-A1.  
XX  
PD 24-SEP-2003.  
XX  
XX 12-APR-2002; 2002EP-00008400.  
XX  
XX 22-MAR-2002; 2002JP-00137785.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-723558/69.  
XX  
XX N-PSDB; ADM03646.  
XX  
PT New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX

Claim 1; SEQ ID NO 4774; 305pp; English.

PS The invention relates to a novel human polynucleotide and the encoded  
XX polypeptide. A polynucleotide of the invention AD06202-AD06773 is useful  
CC therapy. An oligonucleotide of the invention AD06202-AD06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides AD06202-AD06773 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins AD06202-AD06773 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.

XX Sequence 707 AA;

Query Match 30.5%; Score 1559; DB 7; Length 707;

Best Local Similarity 37.1%; Pred. No. 4.2e-90;

Matches 364; Conservative 94; Mismatches 216; Indels 306; Gaps 13;

QY 1 MLLWVILLVAPVSGQFARTPTPILOPQVTVFQGERVLTCKGFRFPYSPQ-KTKVYH 59  
Db 1 MLLWVILLVLTGREGVAPKAVILLNPWSTAFKGEKVALICSSIGHSLAQGDYVYH 60  
QY 60 RYLKGEILRETPDNILOVESEYRCQAGSPSSPVHLDSSASILLQAPLSVEGDSV 119  
Db 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSUAVHVEFSPDWLILQALHPVEGDV 116  
QY 120 VLRCRAKAEVLTNNITVKNQDNVLAFLKRTDFHPIACLKDKNGAYRCTGYKESC---CPV 176  
Db 117 ILRCQKDNKNTKQVYKDKGQKLPNSYNLEKITVNSVSRDMSKYHCTAYRKFYILDIEV 176  
QY 177 SNTVQIQVQEPTRPVLRASSPQISGNPVLTCTQSLERSDPLFRFRDRDQTLG 236  
Db 177 TSKPLNIQVQLFHLVLRASSSTPIEGSPMTLTCTQSLSPQRPVQLQFLSRDSQTLG 236  
QY 237 LCHSLSPNQITAMWSKDSGFYKAAWTHPSVLSDSPPSWIQVQVLPASHPVLTLSPEKA 296  
Db 237 LGWSRSPKQIPAMWTDSSGYWCEVETVTHSKRSLSQIRVQ----- 281  
QY 297 LNPFGTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERGASISFSTTENSNGYYCT 356  
Db 282 ----- 281  
QY 357 ADNLGAKPKSKAVSLVTVVPSHPVLNLSPPEDLIEGAKVTLHCEAQRGSLPILYQFHH 416  
Db 282 -----RVPSVNVNLEIRPTGQLIEGENWNLICVAGSGGVTFESWK 324  
QY 417 ED--AALERSANSAGGVAISFLTAHSGNYCTADNGFGPQSKAVSLSTVVPVHPV 474  
Db 325 EGRVRSIGRKT-----QRSLLAELH-----V 345  
QY 475 LTLSSAALTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGVRSFSLTEG 534  
Db 346 LTVKESDA----- 353  
QY 535 HSGNYCTADNGFGPQSKAVSLVTVVPSHPVLNLSPPEDLIEGAKVTLHCEAQRGSP 594  
Db 354 --GRYCAADNVHSPILSTVIRVTRIPVSHVLTFRAPRAHTVVDLLEHCESLRGSP 411  
QY 595 PILYFWYHEDVTLGSSAPSGGEASPNLSLTAHSGNYCEANGLVAQHSIDTISLVIV 654  
Db 412 PILYFWYHEDVTLGSSAPSGGGASPNLSLTAHSGNYSCDADNGLAQHSHGVSLRVTV 471  
QY 655 PVSRPILTFRAPRAQAVVGDLEHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFN 714  
Db 472 PVSRPILTFRAPRAQAVVGDLEHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFN 531  
QY 715 LSLTTHSGIYSCADNGLAQHSHGVSLRVTVLTAHSGNYCEANGLVAQHSIDTISLVIV 774  
Db 532 LSLTT----- 536  
QY 775 ALRGSPLILYRFFHEDVTLGNRSFSGASNLSLTAHSGNYSCADNGLAQHSHGVSLRVTV 834

Db 537 -----EHSNGYSCADNGLAQHSHGVSLRVTV 559  
QY 835 LYITGLTANSGDPFATGVAGCLLSIAGLAAGALLLYCWLRSKAGRP----- 881  
Db 560 LNVITGTSRNTGLTAAGITGLVLSILVLAALH---YARARRKPGGLSATGTSHP 616  
QY 882 --ASDPARS-PSDSQEPYTHVPAWEELQPVVTNANPRGENVYSEVRILQEKKHAV 938  
Db 617 SECEPSSSRPRIDPOEPFTHSKPLAPMELEPMYNNVPCDSNPIYSQIWSIQTRENSA 676  
QY 939 ASDPRHLNRKSGPIIYSEVK 958  
Db 677 NCPMMHQHEBELTVLYSELK 696

RESULT 11

AAB82316

ID AAB82316 standard; protein; 734 AA.

XX AAB82316;

XX 23-JUL-2001 (first entry)

XX Human immunoglobulin receptor IRTA3 protein.

XX Immunoglobulin superfamily receptor translocation associated; IRTA3;  
KW human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma; myeloma;  
KW B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

XX Homo sapiens.

XX WO200138490-A2.

XX 31-MAY-2001.

XX 28-NOV-2000; 2000WO-US032403.

XX 29-NOV-1999; 99US-0168151P.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Dalla-Favera R;

XX WPI; 2001-355921/37.

XX N-PSDB; AAF30953.

XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor  
PT Translocation Associated proteins, used to treat B cell malignancies  
PT including lymphomas and multiple myeloma.

XX Claim 4; Fig 18C-1-18C-2; 72pp; English.

XX The present sequence is that of the novel human immunoglobulin receptor,  
CC immunoglobulin superfamily receptor translocation associated protein 3  
CC (IRTA3), an Fc receptor involved in the pathogenesis of lymphoma and  
CC melanoma. Efforts to identify genes involved in chromosomal aberrations  
CC affecting band 1q21 in multiple myeloma and B cell lymphoma led to the  
CC discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a  
CC novel subfamily of related receptors within the immunoreceptor family. 3  
CC additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were  
CC subsequently identified, which are also members of this novel subfamily.  
CC The IRTA genes display a specific pattern of expression in mature B  
CC cells. IRTA3 is expressed in GC centrocytes and in perfollicular cells,  
CC which may include lymphoblasts and memory cells. This is analogous to  
CC IRTA2 expression. The invention provides IRTA nucleic acids and proteins,  
CC and antibodies directed to an epitope of an IRTA protein. Methods are  
CC claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal  
CC rearrangement using a nucleic acid molecule that specifically hybridises  
CC with a unique sequence of human IRTA1-5; and treating a subject having a  
CC B cell cancer by administering an anti-IRTA antibody or an antisense  
CC oligonucleotide that specifically hybridises to IRTA mRNA so as to  
CC prevent overexpression of IRTA protein and hence to arrest cell growth or  
CC induce cell death of cancer cells expressing IRTA. The B cell cancer is



```
QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESC---CPV 176
Db 117 ILRCQKDNKNTKQVYKDGKQLENSVNRDNLKITVNSVRDNLKXCTAYRKFYILDIEV 176
QY 177 SSNTVKIQVEEPTFRPVLRASSFPISGNPVLTCETQLSLERSDVPLRFRFRDDQTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPVQLQFSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGFYWCXAAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKA 296
Db 237 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ-----281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTENSNGYYCT 356
Db 282 -----281
QY 357 ADNLGAKPSKAVSLSVTVPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Db 282 -----RVPVSNVNLIRPTGGQLIEGENMVLICSAVQSGTGTFTFSWHK 324
QY 417 ED--AALERRANSAGGVAISFSLTAHSGNYCTADNCGFGPORSKAVSLSVTVPSHPV 474
Db 325 EGRVSLGRKT-----ORSLLAELH-----V 345
QY 475 LTLSSAEALTPEGATVTLHCEVORGSPQLLYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 346 LIVKESDA-----353
QY 535 HSGNYCTADNCGFGPORSSEVSLFVTVVPSRPIILTRVPRAQAVVGDLLHCEAPRSP 594
Db 354 --GRYCAADNVHSPILSVIRVTRIPVSHPVLTFRAPRAHTVVGDLLEHCESLRGP 411
QY 595 PILYFYHEDVTLGSSAPSGCEASPNLSLTAHSGNYSCNANGIYVAQHSPTISLSTIV 654
Db 412 PILYFYHEDVTLGNSSAPSGGASPNLSLTAHSGNYSCDADNGLGAHSHGVSLRVTV 471
QY 655 PVSRLPILTRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASPN 714
Db 472 PVSRLPILTRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASPN 531
QY 715 LSLTTHSGIYCEADNGLGAQRSEMVLKAVPSRPIILTRAPGTHAAVGDLLHCE 774
Db 532 LSLTT-----536
QY 775 ALRGSPILYFYHEDVTLGNSSPSGGASNLSLTAHSGNYSCBNDNGLGAQRSETV 834
Db 537 -----EHSNGYSCBNDNGLGAQRSKVTV 559
QY 835 LYITGLTANRSGPFATGVAGGLISLAGAALLLYCWL-SRKAGRP-----881
Db 560 LNVGTGSRNRTGLTAAGITGLVLSILVLAALAAALLH--YARARRKPGGLSATGTSSHSP 616
QY 882 --ASDPARS-PSDSDSQEPTYNVPABELOPVYTNANRGENVYVSEIRITOEKKHAV 938
Db 617 SECQEPSSRPSRIDPQETHSKPLAPMELEPMYSNVNFCDSNPITYSOWISQHTKNSA 676
QY 939 ASDPRLHNRKGPSIIYSEVK 958
Db 677 NCPMMQHEHELTLYSELK 696
```

RESULT 13

```
ID ADL06557
XX ADL06557 standard; protein; 733 AA.
AC
XX
XX 20-MAY-2004 (first entry)
DE Human tumour-associated antigenic target (TAT) polypeptide #56.
XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.
DB 281 -----RVPVSNVNLIRPTGGQLIEGENMVLICSAVQSGTGTFTFSWHK 323
```

```
XX Homo sapiens.
OS WO2004016225-A2.
XX
PN 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
XX (GETH ) GENENTECH INC.
PA Desauvage FJ, Frantz G, Hillian KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
PI
XX MPI; 2004-257144/24.
DR N-PSDB; ADL06478.
DR
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
PS Claim 2; SEQ ID NO 137; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT polypeptide of the invention.
XX
SQ Sequence 733 AA;
```

Query Match 30.4%; Score 1556.5; DB 8; Length 733;  
Best Local Similarity 37.0%; Pred. No. 6.4e-90;  
Matches 363; Conservative 95; Mismatches 215; Indels 307; Gaps 13;

```
QY 1 MLLWLLVLAIPVSGQFARTPRPIIFLOPPPTVTFQGRVTLTKGFRFYSQ-KTKWYH 59
Db 1 MLLWLLVLLITPGRQSGVAPKAVLLNPPSTAFKGEKVALICSSISHSLAQGDTYWH 60
QY 60 RYLKKEILRETPDNTILEVQESGEYRCQAQGPLSPVHLDFSSASLILQAPLSVFEQDSV 119
Db 61 ---DEKLLIKHD--IQITEPGNYCKTRGSSLSDAHVFEFSPDWLILQALHPVEGDNV 115
QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESC---CPV 176
Db 116 ILRCQKDNKNTKQVYKDGKQLENSVNRDNLKITVNSVRDNLKXCTAYRKFYILDIEV 175
QY 177 SSNTVKIQVEEPTFRPVLRASSFPISGNPVLTCETQLSLERSDVPLRFRFRDDQTLG 236
Db 176 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPVQLQFSLFRDSQTLG 235
QY 237 LGWSLSPNFQITAMWSKDSGFYWCXAAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKA 296
Db 236 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ-----280
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTENSNGYYCT 356
Db 281 -----280
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Db 170 TSKPLNIQVQELFLHPVLRASSSTIEGSPMLTCTETQSPORPVQLOFSLFRDSQTIG 229  
QY 237 LGWSLSPNFOITAMWSKDSGFYCKAAATPHSVISDSRSPWQIQVQIPASHPVLTLSPKA 296  
Db 230 LGWSRSPRIQIPAMWTEDSGYWCVEIVTHSIKRSLSRQIRVQ----- 274  
QY 297 LNFEGTKVTLHCETQEDSLRTLYRFYHEGVLPURKSVRCERCASISFSLTTENSQNYCT 356  
Db 275 ----- 274  
QY 357 ADNLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHH 416  
Db 275 -----RVFVSNVNLRIPTGGQILIEGEMVLLICVAGSGTGVTFSSHK 317  
QY 417 ED--AALERRSANSAGVAISFSLTAHSGNYCYCTADNGFGPQRKAVSLSTVTPVSHV 474  
Db 318 EGRVRSLGKRT-----QRSLLAEHL-----V 338  
QY 475 LTLSSAEALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534  
Db 339 LTVKESDA----- 346  
QY 535 HSGNYCYCTADNGFGPQRSEWSLFTVTPVSRPILTLRVPRAQAVGDLLELHCEAPRGSP 594  
Db 347 --GRYYCAADNVHSPILSTWIRTVIPVSHVPLTFRAPRAHTVVGDLLELHCESLRGSP 404  
QY 595 PILYFYHEDVTLGSSAPSGGASPNLSLTAHSGNYSCEANGLVIAQHSOTISLSVTV 654  
Db 405 PILYFYHEDVTLGNSAPSGGASPNLSLTAHSGNYSCEADNGLGASHGVSLRVTV 464  
QY 655 PVSRLPILTRAPAAQAVGDLLELHCEALRGSPILYFYHEDVTLGKISAPSGGASPN 714  
Db 465 PVSRLPILTRAPAAQAVGDLLELHCEALRGSPILYFYHEDVTLGKISAPSGGASPN 524  
QY 715 LSLTTEHSGIYSCADNGLAORSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLELHCE 774  
Db 525 LSLTT----- 529  
QY 775 ALRGSPLILYRPFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLAORSETV 834  
Db 530 -----EHSNGYSCADNGLGASHQSVTV 552  
QY 835 LYITGLTANRSGPFATGAGLLSIAGLAAGLLLYCWLRSRAGKRP----- 881  
Db 553 LNVITGSRNRTGLTAAGITGLVLSILVLAALH---YARARRPGGLSATGTSSHSP 609  
QY 882 --ASDPARS-PSDSDSQEPTTHNVPAWEEQLQPVYTNANPRGENVYSEVRIIQEKKHAV 938  
Db 610 SECEPSSSRPRIDPQEPHSPKPLAPMELEPYSNVNPGDSNPIYSQIWSIQTENSA 669  
QY 939 ASDPRHLRNKGSPIIYSEVK 958  
Db 670 NCPMMHQEHELTIVLYSELK 689

RESULT 15

ID AEM84916 standard; protein; 750 AA.  
XX AC AEM84916;  
XX AC AEM84916;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5165.  
XX DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX KW Homo sapiens.  
XX OS Homo sapiens.  
XX PN WO2004023973-A2.  
XX PD 25-MAR-2004.  
XX PD 281

XX PF 12-SEP-2003; 2003WO-US028227.  
XX PR 12-SEP-2002; 2002US-0410259P.  
XX PR 12-SEP-2002; 2002US-0410260P.  
XX PA (INCY-) INCYTE CORP.  
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitte SJ, Elder LV,  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patry S, Shi X, Suarez CJ;  
XX WIPI; 2004-329368/30.  
XX DR N-PSDB; ACN43568.  
XX DR New diagnostic and therapeutic polynucleotides and polypeptides, useful  
XX PT in diagnosing a condition, disease or disorder associated with human  
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX PT in gene mapping.  
XX PS Claim 27; Page; 190pp; English.  
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides  
XX CC selected from one of the 2722 sequences defined in the specification. A  
XX CC polynucleotide of the invention may have a use in gene therapy. The human  
XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
XX CC used to diagnose a particular condition, disease or disorder associated  
XX CC with human molecules, e.g. cell proliferative disorders,  
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
XX CC disorder, neurological disorders, gastrointestinal disorders, or  
XX CC infections caused by virus, bacteria, fungi or parasite. The dithp  
XX CC molecules may also be used in genetic mapping, in identifying individuals  
XX CC from minute biological samples, in detecting single nucleotide  
XX CC polymorphisms, as molecular weight markers, and for somatic or germline  
XX CC gene therapy. The present sequence represents a dithp protein of the  
XX CC invention. Note: The sequence data for this patent is not represented in  
XX CC the printed specification, but was obtained in electronic format directly  
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
XX SQ Sequence 750 AA;  
Query Match 30.1%; Score 1538.5; DB 8; Length 750;  
Best Local Similarity 36.9%; Pred No. 9.2e-89;  
Matches 362; Conservative 94; Mismatches 211; Indels 313; Gaps 14;  
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCGRFPYSPQ-KTKWYH 59  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCGRFPYSPQ-KTKWYH 60  
QY 60 RYLKREILRETPDNLVEQESGEYECQAGSPVHLDFESSASILLQAPLSVFEQDSV 119  
Db 61 ---DEKLKIKHDKI-QITEPGNYQCKRGSSLSDAVHFSPFDWLLIQLHPVEGDV 116  
QY 120 VLRCRAKABVTLLNNTYTKNDNVLAFLNKRTPDHPHACLKDKNGAYRCTGYKESC---CPV 176  
Db 117 ILRCQCKDNKTHQVYKQKQLPNSVLEKIVNSVSRDNSKYHCTAYRKFIILDIIEV 176  
QY 177 SSNTVKIQVEPFTPRPVLRASSFPISGNPVLTCETQLSLERSDVLPFRFRDQOTIG 236  
Db 177 TSKPLNIQVQELFLHPVLRASSSTIEGSPMLTCTETQSPORPVQLOFSLFRDSQTIG 236  
QY 237 LGWSLSPNFOITAMWSKDSGFYCKAAATPHSVISDSRSPWQIQVQIPASHPVLTLSPKA 296  
Db 237 LGWSRSPRIQIPAMWTEDSGYWCVEIVTHSIKRSLSRQIRVQ----- 281  
QY 297 LNFEGTKVTLHCETQEDSLRTLYRFYHEGVLPURKSVRCERCASISFSLTTENSQNYCT 356  
Db 281 ----- 281







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:27:40 ; Search time 32.7345 Seconds  
(without alignments)  
2227.987 Million cell updates/sec

Title: US-09-724-254A-41  
Perfect score: 5116  
Sequence: 1 MLLWVILLVLPVSGGFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3787.5	74.0	1248	4	US-09-949-016-10595
2	3787.5	74.0	1248	4	US-09-949-016-10596
3	412	8.1	4391	4	US-10-006-011A-2
4	386	7.5	261	4	US-09-245-764-7
5	359	7.0	1709	4	US-09-949-016-10503
6	351.5	6.9	738	3	US-08-478-208-32
7	351.5	6.9	738	4	US-09-336-536-73
8	344.5	6.7	738	6	5264554-2
9	344.5	6.7	738	6	5264554-2
10	316.5	6.2	698	2	US-08-602-725-36
11	316.5	6.2	702	4	US-09-949-016-6484
12	316.5	6.2	734	2	US-08-389-459A-17
13	316.5	6.2	734	3	US-08-987-867A-17
14	316.5	6.2	740	4	US-09-949-016-8168
15	305.5	6.0	254	2	US-08-667-939A-3
16	305.5	6.0	254	4	US-08-433-123-3
17	304.5	6.0	254	2	US-08-667-939A-2
18	304.5	6.0	254	4	US-08-433-123-2
19	294.5	5.8	642	1	US-08-217-299-1
20	293	5.7	233	2	US-08-667-939A-6
21	293	5.7	233	4	US-08-433-123-6
22	292.5	5.7	254	2	US-08-667-939A-9
23	292.5	5.7	254	4	US-08-433-123-9
24	292	5.7	233	2	US-08-667-939A-5
25	292	5.7	233	4	US-08-667-939A-8
26	292	5.7	233	4	US-08-433-123-5
27	292	5.7	233	4	US-08-433-123-8

28	290	5.7	315	4	US-09-949-016-11121	Sequence 11121, A
29	290	5.7	315	4	US-09-949-016-11122	Sequence 11122, A
30	288.5	5.6	254	2	US-08-667-939A-4	Sequence 4, Appli
31	288.5	5.6	254	4	US-08-433-123-4	Sequence 4, Appli
32	286	5.6	233	2	US-08-667-939A-7	Sequence 7, Appli
33	286	5.6	233	4	US-08-433-123-7	Sequence 7, Appli
34	285.5	5.6	254	2	US-08-667-939A-1	Sequence 1, Appli
35	285.5	5.6	254	4	US-08-433-123-1	Sequence 1, Appli
36	285	5.6	1395	3	US-09-540-245A-15	Sequence 15, Appl
37	284	5.6	1070	4	US-09-961-403-3	Sequence 3, Appli
38	283	5.5	917	1	US-08-245-295-2	Sequence 2, Appli
39	283	5.5	917	1	US-08-481-130-2	Sequence 2, Appli
40	283	5.5	917	1	US-08-656-384A-2	Sequence 2, Appli
41	283	5.5	917	1	US-08-485-604-2	Sequence 2, Appli
42	283	5.5	917	2	US-08-487-595-2	Sequence 2, Appli
43	275	5.4	197	3	US-08-788-954-2	Sequence 2, Appli
44	275	5.4	203	2	US-08-667-939A-20	Sequence 20, Appl
45	275	5.4	203	4	US-08-433-123-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10595  
; Sequence 10595, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10595  
; LENGTH: 1248  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10595

Query Match	74.0%	Score	3787.5	DB	4	Length	1248
Best Local Similarity	97.2%	Pred. No.	2.9e-317				
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Gaps	2						
QY	1	MLLWVILLVLPVSGGFARTPRIIIFLOPPWTTVFOGERVTLTKGFRFYSPOKTKWYHR	60				
Db	476	MLLWVILLVLPVSGGFARTPRIIIFLOPPWTTVFOGERVTLTKGFRFYSPOKTKWYHR	535				
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV	120				
Db	536	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV	595				
QY	121	LRCAKAEVTLNNTIYKNDNVLAFLNKRITDFHIFHACLKNGAYRCTGYKESCCPVSSNT	180				
Db	596	LRCAKAEVTLNNTIYKNDNVLAFLNKRITDFHIFHACLKNGAYRCTGYKESCCPVSSNT	655				
QY	181	VKIQVEPTRPVLRASSFPQISGNVTITCTQLSLERSDVLRFRRFDDDTGLGWS	240				
Db	656	VKIQVEPTRPVLRASSFPQISGNVTITCTQLSLERSDVLRFRRFDDDTGLGWS	715				
QY	241	LSPNFOITAMWSKDSGFYKCAATMPHSVTSIDSPRSWIOVOIPASHPVLTLSPKALNFE	300				
Db	716	LSPNFOITAMWSKDSGFYKCAATMPHSVTSIDSPRSWIOVOIPASHPVLTLSPKALNFE	775				
QY	301	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGYCTADNG	360				

Db	776	GTQVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYCTADNG	835
Qy	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA	420
Db	836	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA	895
Qy	421	LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVNLSSA	480
Db	896	LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVNLSSA	955
Qy	481	EALTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
Db	956	EALTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	1015
Qy	541	CTADNGFGPQRSSEVSVLFTVTVPSRPILTLRPVRAQAVVGDLELHCEAPRGSPPILYWF	600
Db	1016	CTADNGFGPQRSSEVSVLFTVTVPSRPILTLRPVRAQAVVGDLELHCEAPRGSPPILYWF	1073
Qy	601	YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI	660
Db	1074	YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI	1133
Qy	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT	720
Db	1134	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT	1174
Qy	721	HSGIYSCDADNGLEAQRSEMTLKV	746
Db	1175	HSGIYSCDADNGLEAQRSEMTLKV	1200
RESULT 2			
US-09-949-016-10596			
; Sequence 10596, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CLO01307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 10596			
; LENGTH: 1248			
; TYPE: PRT			
; ORGANISM: Human			
US-09-949-016-10596			
Query Match			
Best Local Similarity 74.0%; Score 3787.5; DB 4; Length 1248;			
Matches 725; Conservative 0; Mismatches 0; Indels 21; Gaps 2;			
Qy	1	MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTWYHR	60
Db	476	MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTWYHR	535
Qy	61	YLKGEILRETPDNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV	120
Db	536	YLKGEILRETPDNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV	595
Qy	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT	180
Db	596	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT	655
RESULT 3			
US-10-006-011A-2			
; Sequence 2, Application US/10006011A			
; Patent No. 6821947			
; GENERAL INFORMATION:			
; APPLICANT: Iozzo, Renato V.			
; TITLE OF INVENTION: Endorepellin: methods and compositions			
; TITLE OF INVENTION: for inhibiting angiogenesis			
; FILE REFERENCE: 8321-95			
; CURRENT APPLICATION NUMBER: US/10/006,011A			
; CURRENT FILING DATE: 2001-12-04			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 4391			
; TYPE: PRT			
; ORGANISM: human			
US-10-006-011A-2			
Query Match			
Best Local Similarity 8.1%; Score 412; DB 4; Length 4391;			
Matches 221; Conservative 131; Mismatches 422; Indels 180; Gaps 44;			
Qy	23	PIIFLOPPWTVFQGERVTLCKGFRFYSPQK-TKWYHRYLKGKEILRETPDNIL-----E	76
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Qy	77	VOESGEYRCQAGSPVHLDFSSASLILQAPLSV	114
Db	2688	VADSGEYVCRANNIDALEASIVSVPSAGSFPAGSSMPRIRESSS-----HVA	2739
Qy	115	EGDSVVLRCRAKAEVTLNNTIYKNDNVLA--FLNKRTPDHPHACLKONGAYRC-----T	167

Db 2740 EGETLDLNCVVPGQAHAQVTHKRGGLSPSHHQTRGSRRLRLHHVSPADSGEYVCRVMGSS 2799  
Qy 168 GYKESCCPV---SNTVKIQOEBEFTFPLVR--ASSFOPTISGNPVTLTC-----ETQLS 216  
Db 2800 GPLEASVLVTEASGSSAVHPAPGGAPPIETIESSSRVAEGQTLDLKCVPGQAHAQVT 2859  
Qy 217 LER---SDVPLRFRFRDDQTLGLGWSLSPNQITAMMSKSGFYWK-----AATMPSHV- 269  
Db 2860 WHKRGGLPARHGVH-----GPLLRLNQVSPADSGEYSCQVTGSSGTLEASVL 2907  
Qy 270 ISDSPRWIQOIPASHPVLTLSPKALNPGTKVTLHCETOEDSLRFLRYFYHEG---VP 327  
Db 2908 VTIEPSPGPIAPGLAQPIYIEASSHVTEGQTLNLCVVPGQA-HAQVTWYKRGGLSP 2966  
Qy 328 LRHSVRCERGASISFSLTT-ENGSGNYCTADNGLGAKPSKAVLSLTVPVSH----- 379  
Db 2967 ARHOT---HGSQRLHLVSPADSGEYVCRASGPG--PEGEASFTVTPPSESSYRLR 3020  
Qy 380 -PVLNLSPEDLIEGAKVTLHCQAQSGSLPILYQFIHEDDAALERRSANGGVAISFSL 438  
Db 3021 SPVISIDPPSSTVOGQDASPKLIHDAAPISLEWTKRNOELEDNVRHISPNGSIIITVG 3080  
Qy 439 T-AHSGNYCTADNGCPQRSKAVLSITVPVSHPVLTLSSEALTFEGATVTLHCEVQ 497  
Db 3081 TRPSNHGTYRCVASNAYGVAQS-VVNLVSHGPPT--VSVLPEGPVWVKVGAVTLEC-VS 3136  
Qy 498 RGSQILYQFYHEDMPLWS--SPTSVGRVSFSPSLTEGH-----SGNYCYTA 543  
Db 3137 AGEPR-----SSARKTRISSTPA-KLEORTYGLMDSHAVLQISSAKPSDAGTYVCLA 3187  
Qy 544 DNGFPORSEVSLFVTPVSRPILTLRVPRQAVV--GDLELHCEAPRGSPPILYW-- 599  
Db 3188 QNALGTAQKQVEVIVDTGAMAPGAQVQAEAEALTVEAGHTATLRCSATGSPAPTIHWSK 3247  
Qy 600 -----FYHEDVTLGSSASPGGEASFNLSITAEHSGNYSCEANGLVQAQSD-TISLSV 652  
Db 3248 LRSPLPQHR-----LEGDTLIIPVAQDQSGQYICNATS--PAGHAETIILHV 3295  
Qy 653 IPVSRPILTFRAPRAQAVGDLELHCEALRGSSPILY-WFYHEDVTLGKISAPSGGA 711  
Db 3296 ESP---PYATVPBHASVQAGETVQLOCLA-HGTPPLTFQW-----SRVSSLPGR 3343  
Qy 712 SPNLSL-----TTEHSGIYSCDADNGLEAQRSEMVTLKVAPVSRPVLTLRAPGTHA-- 763  
Db 3344 TARNELLHFAAPEDSGRYCRVTNKVGSAAEPAQLLVQGPGLPATSIPAGSTPTVQ 3403  
Qy 764 -----AVGDLELHC--BALRGSPILYRPFHEDVTLGNRSSPGSGASLNLSTAEH 813  
Db 3404 VTPQLETKSIGASVEFHCAPVSDQGTQL---RWFKEGGQLPPGHVSQDGVLRIQNLQDSC 3460  
Qy 814 SGNYSCEADNGLG-AORS-ETVTLIYITGLTANRSGPFATGVAGLLSGLAAG 865  
Db 3461 QGYTICQHGFGWKAQASQILVQALFSLVILNIRTSVQTVVGVHAFBECLALG 3514

## RESULT 4

US-09-245-764-7

; Sequence 7, Application US/09245764

; Patent No. 6675105

; GENERAL INFORMATION:

; APPLICANT: Hogarth, P. Mark

; APPLICANT: Powell, Maree S.

; APPLICANT: McKenzie, Ian F.C.

; APPLICANT: Maxwell, Kelly F.

; APPLICANT: Garrett, Thomas P.J.

; APPLICANT: Epa, Vidana

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS

; FILE REFERENCE: 4102-4

; CURRENT APPLICATION NUMBER: US/09/245,764

; CURRENT FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: 60/099,994

; EARLIER FILING DATE: 1998-09-11

; EARLIER APPLICATION NUMBER: 60/073,972

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 261

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-245-764-7

Query Match 7.5%; Score 386; DB 4; Length 261;

Best Local Similarity 35.7%; Pred. No. 5.9e-25;

Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;

Qy 20 TPRPIIQLPQWTVTFQGERVTLTKCGFRFVSPQKTKWYHRYLKKEILRETPD--NILE 76

Db 1 TTKAVITLQPPWVSFQEEVTLHCEVLHLPGLSSSTQWFVN--GTATQTSTPSPRITSAS 58

Qy 77 VQESGEYRCQAQSGSLSSPVHLDFSSASLILQAPLSVF-EGDSVYLCRAKAEVTLNNTI 135

Db 59 VSDSGEYRCQGLSGRSDPIQLEIHRGWLLQLQVSRVFTGEPLALRCHAWKDKLVYNVL 118

Qy 136 YKDNVLAFLNKRTDTHI PHACLKDNCAIYRCTGYKESCCPVSNVTVKIQOEBEFTFPLVR 195

Db 119 YYRNGKFKFFHMSNLTKTNISHNGTYHCSGMGKH--RYTSAGISVTVKELFPAPVLN 176

Qy 196 ASSFQIP-ISCNPVTLTCETOLSERSDPLRFRFRDDQTLGLCWSLSPNQITAMMSKD 254

Db 177 ASVTSPLLEGNLVTLSCEITKLLKQRPGLQLYFYFGMSKTL-RGRNTSSEYQILTARRED 235

Qy 255 SGFYCKAAATMPHSVSDSPRSWIQV 280

Db 236 SGLYWCEAATEDGNVLKRSPELELQV 261

## RESULT 5

US-09-949-016-10503

; Sequence 10503, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10503

; LENGTH: 1709

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-10503

Query Match 7.0%; Score 359; DB 4; Length 1709;

Best Local Similarity 23.0%; Pred. No. 2.5e-21;

Matches 231; Conservative 113; Mismatches 408; Indels 254; Gaps 50;

Qy 10 LAPVSGQFARTPRPIIFL-----QPPWTTFV-QGSERVTLTKGFFYSPQTKWYHRY 61

Db 413 LTPVLAFTAQAGLGHILHCSVVSEPLATLVLSHGHIILASTSGSDHSPR----PSGT 468

Qy 62 LGKEILR-ETPDNILEVOESGEYRCQAQSGSLSPVHLDF--SSASLILQAPLSVPEGDS 118

Db 469 SGPNSLRLEIRD--LBETDSGEYKCSATNSLGNATSLDTPHANAARLLISPAAEWEGQA 526



Patent No. 6406884  
 GENERAL INFORMATION:  
 APPLICANT: Leiby, K.  
 APPLICANT: McKay, C.  
 APPLICANT: Bosson, S.  
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
 FILE REFERENCE: 7853-144  
 CURRENT APPLICATION NUMBER: US/09/336,536  
 CURRENT FILING DATE: 1999-06-18  
 NUMBER OF SEQ ID NOS: 75  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 73  
 LENGTH: 738  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-336-536-73

Query Match 6.9%; Score 351.5; DB 4; Length 738;  
 Best Local Similarity 22.6%; Pred. No. 2.9e-231;  
 Matches 177; Conservative 120; Mismatches 336; Indels 151; Gaps 33;  
 259 WCAATMPHSPVISDSRPSRWIQVQP-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLPDWTVQNGKNL 297  
 Db 5 WCAQATM-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLPDWTVQNGKNL 53  
 298 N-----FEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTE-----ASHPVLTLSPKAL 348  
 Db 54 TLOCFADVSTTSHVKPOHQL-----FYKODVLF-----YNISSMKSTESYFIPE 98  
 349 ----NSGNYCTADNGLGAKPSKAVSLSTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQ 404  
 Db 99 VRIYDSGTYKCTVIVNKKETTAAYQLLVE-GVPSRPTLDKKEAI--QGGIVRVNCSVP 155  
 405 RGSPLILYOPH-----HEDAALERSANSAGGVAISFSLTAHSG--NYCTAD--NGFG 455  
 Db 156 EERAPIHTTEKLELNEKMKVKLRKNSRDQNFVLEFPVEQDRVLSFRQARIISGIH 215  
 456 PQRS----KAVLSGITVPVSHPVLTLSAEALTFEGATVTLHCEVQ-----RGSPOILYQF 507  
 Db 216 MOTSESTKSELVTVTESFSTPKFHSPT-GMINEGAQLHKICTQVTLHAEFPEIIQ- 273  
 508 YHEDMPLWSSTPSVGRVVSFSLTEGHSNGNYCTADNFGPQRSEVSLFVTVP--VSR 565  
 Db 274 --KDKAIVAHNRHGNKAVYSVMAMVE-HSGNYTCKESS--RISKVSSIVVNITELFSK 327  
 566 PILTLRVRAQAVVGDLLHCEALRGSPPIILYFVHEDVTLGSSAPSGEASFNLSLT 625  
 Db 328 PELESSFTHLQD--GERLNLSCSIP-GAPPANFTIQKEDTIVSQTO-----DFTKIAS 377  
 626 AEHSNGYSCNANGLVAQHSDDTISLSVIVPVSRLPILTFRAPRAQAVVGDLLHCEALRG 685  
 Db 378 KSDSGTYICTAGIDKVVKSNTVQIVVCEMLSQPRISYDA-QPEVIKGTIEVRCESISG 436  
 686 SSPILYFVHEDVTLGKISAPSGGASFNLSLTHSGIYSCADN--GLEAQRSEMTVL 743  
 Db 437 TLPISVQLLTKTSKLENSTKNSNDPAVFKDNPTEDEVE--YQCVDNCHSHAKMLSEVLRV 494  
 744 KVAVPVSRLPILTRAPGTHAAVGDLLHCEALRGSPPIILYFVHEDVTLGNSSPSGGA 803  
 Db 495 KVTAPVDEVOISILSKV--VESGEDIVLQCAVNEGSGPIYKYRE-----KEGKFPYQM 548  
 804 SLNLS-----LTAHSGNYSC-----EADNGLGAQRSEMTVLYITGLTANRSGPFATG 851  
 Db 549 TSNATQAFWTKQKASKEQEYCTAFNRANHASSVPSRKLTVRVI-LAPMKGLIAVV 607  
 852 VAGGLISIAGLAGALLLYCWLRSKAGRK-----PASDPARSPSDSDSQEPTVYHNPVWEE 907  
 Db 608 IIGVITALLIIAA-----KCYFLRKAKAKOMPVEMSRPAVPLNLSNKKMSDPNMEANSH 662  
 908 -----LQPVYTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSE 956  
 Db 663 YGHNDVNRHAMKPINDNKEPLNSDVQYTEVQV-----SSAESKDLGKKDTETVISE 715

957 VKVA 960  
 Db 716 VRKA 719  
 RESULT 8  
 5264554-2  
 Patent No. 5264554  
 APPLICANT: Newman, Peter J.  
 TITLE OF INVENTION: PLATELET CELL ADHESION MOLECULE AND  
 VARIANTS THEREOF  
 NUMBER OF SEQUENCES: 2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/466,140  
 FILING DATE: 19-JAN-1990  
 SEQ ID NO:2:  
 LENGTH: 738  
 5264554-2

Query Match 6.7%; Score 344.5; DB 6; Length 738;  
 Best Local Similarity 22.4%; Pred. No. 1.2e-20;  
 Matches 173; Conservative 121; Mismatches 349; Indels 131; Gaps 31;  
 259 WCAATMPHSPVISDSRPSRWIQVQP-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLPDWTVQNGKNL 297  
 Db 5 WCAQATM-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLPDWTVQNGKNL 53  
 298 N-----FEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTE-----ASHPVLTLSPKAL 348  
 Db 54 TLOCFADVSTTSHVKPOHQL-----FYKODVLF-----YNISSMKSTESYFIPE 98  
 355 CTADNGLGAKPSKAVSLSTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQF 414  
 Db 109 CTIVNKKETTAAYQLLVE-GVPSRPTLDKKEAI--QGGIVRVNCSVPPEEKAPIHFTI 165  
 415 H-----HEDAALERSANSAGGVAISFSLTAHSG--NYCTAD--NGFGPQRS--KAV 462  
 Db 166 EKLELNEKMKVKLRKNSRDQNFVLEFPVEQDRVLSFRQARIISGIHMTSESTKSE 225  
 463 SLGITVPVSHPVLTLSAEALTFEGATVTLHCEVQ-----RGSPOILYQFVHEDMPLWS 517  
 Db 226 LVTVTESFSTPKFHSPT-GMINEGAQLHKICTQVTLHAEFPEIIQ--KDKAIVAH 281  
 518 STPSVGRVVSFSLTEGHSNGNYCTADNFGPQRSEVSLFVTVP--VSRPILTLRVRA 575  
 Db 282 NRHGNKAVYSVMAMVE-HSGNYTCKESS--RISKVSSIVVNITELFSKPELESSFTHL 337  
 576 QAVVGDLLHCEALRGSPPIILYFVHEDVTLGSSAPSGEASFNLSLTHSGIYSC 635  
 Db 338 DG--GERLNLSCSIP-GAPPANFTIQKEDTIVSQTO-----DFTKIASKDSGTICT 387  
 636 ANGLVAQHSDDTISLSVIVPVSRLPILTFRAPRAQAVVGDLLHCEALRGSPPIILYFV 695  
 Db 388 AGIDKVVKSNTVQIVVCEMLSQPRISYDA-QPEVIKGTIEVRCESISGTLPIISYQLLK 446  
 696 EDVTLGKISAPSGGASFNLSLTHSGIYSCADN--GLEAQRSEMTVLKVAVPVSRPV 753  
 Db 447 TSKVLENSTKNSNDPAVFKDNPTEDEVE--YQCVDNCHSHAKMLSEVLRVKVIAPVDE 504  
 754 LTRAPGTHAAVGDLLHCEALRGSPPIILYFVHEDVTLGNSRSPSGGASLNL 808  
 Db 505 ISILSKV--VESGEQIVLQCAVNEGSGPIYKYRE-----KEGKFPYQMTSNATQAFWT 558  
 809 ---LTAHSGNYSC-----EADNGLGAQRSEMTVLYITGLTANRSGPFATGAGLLSIAG 861  
 Db 559 KQASKEQEYCTAFNRANHASSVPSRKLTVRVI-LAPMKGLIAVVIIIGVITALLI 617  
 862 LAAGALLLYCWLRSKAGRK-----PASDPARSPSDSDSQEPTVYHNPVWEE----- 907  
 Db 618 IAA-----KCYFLRKAKAKOMPVEMSRPAVPLNLSNKKMSDPNMEANSHYGHNDVNRH 672  
 908 -LQPVYTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA 960  
 Db 908 -LQPVYTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA 960

Db 673 AMKPINDNKEPLNSDVQYTEVQV-----SSAESHKDLGKDKTETVYSEVRKA 719

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RESULT 9
5264554-2
; APPLICANT: Newman, Peter J.
; TITLE OF INVENTION: PLATELET CELL ADHESION MOLECULE AND
; VARIANTS THEREOF
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/466,140
; FILING DATE: 19-JAN-1990
; SEQ ID NO:2
; LENGTH: 738
5264554-2
Query Match 6.7%; Score 344.5; DB 6; Length 738;
Best Local Similarity 22.4%; Pred. No. 1.2e-20;
Matches 173; Conservative 121; Mismatches 349; Indels 131; Gaps 31;
QY 259 WCKAATMPHSVSDSPRSVIOVQIP-----ASHPVLTLSPKAL 297
Db 5 WQAQATM-----WGLVLLTLLCSSLEGOENSTINSVDMKSLPDWTQVGNKL 53
QY 298 N---FEGTKVTLHCTEQDSRLTYRPHYHGVPLRHKSVCRCGASISFSLTTSNGYY 354
Db 54 TLQCFADVSTTSHVKPQHQL-----FYKDDVLFYNNVSMKSTESYFIPVRIYDSGT 108
QY 355 CTADNGLGAKPSKAVSLSTVPSVSHPVNLSPEDLIFEGAKVTLHCEAQRGLPILYQF 414
Db 109 CTVIVNKKETAYEQLLVE-GVPSRVLTKKEAI--OGGIVRVNCSVPEKAPIHFTI 165
QY 415 H----HEDAALERRSANSAGGVAISFLTAHSG---NYYCTAD--NGFPQRS---KAV 462
Db 166 EKLELNKVKVLRKNSRDQNFVLEFPVEQDRVLSFRCQARIISGIHMOTSESTKSE 225
QY 463 SLSITVPVSHPVVTLASAALTEGATVTLHCEVQ-----RGSPLLQFYHEDMPLWS 517
Db 226 LVTVTESFSPKPHISPT-GMIMEGALHKTCTIQTHTLAQEPPEIIQ---KDKAIVAH 281
QY 518 STFSVGRVSFSLTEGHSNGYCTADNGFGPORSWSLFTVP--VSRPILTLRVPPRA 575
Db 282 NRGNKAVYSVMWVZ-HSGNYTKVYESS---RISKVSSIVNITELFSKPELESFTHL 337
QY 576 QAVVGDLELHCEAPRGSPPILYFWFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCE 635
Db 338 DG--GERLNLSCSIP-GAPPANFTIQEDTIVSQIQ-----DFTKIASKSDSGTYICT 387
QY 636 ANGLVAQHSDDTISLVIVPVSRPILTFRAPRAQAVVGDLELHCEALRGSSPILYWFYH 695
Db 388 AGIDKVVYKSNVTQIVVCEMLSPISYDA-QEVINGQTIEVKRCISIGTLFISQLLK 446
QY 696 EDVTLGKISAPSGGASFNLSLTHSGIYSCADN--GLEAORSEWTLKAVVPSRPV 753
Db 447 TSKVLENTKNSNDPAVKDKNPTEDE--YQCVADNCHSHAKMLSEVLVKVIAPVDEVQ 504
QY 754 LTLRAPGTHAAVGDLELHCEALRGSPILYRPFHEDVTLGNRSSPSGGASINLS----- 808
Db 505 ISILSSKV-VESGQIVLQCAVNRQSGPITYKYFE-----KEGKPPYQMTSNATQAFWT 558
QY 809 ---LTAHSGNYSK---EADNGLGAORSETVTLITGLTANRSGPFPATGAGLLSIAG 861
Db 559 KQAKSKOEGBYYCTAFNRANHASSVPSKILTVRI-LAPWKGLIAVVIIGVIALLI 617
QY 862 LAAGALLLYCWLRSKAGRK-----PASDPARSPSDSDQEPYTHNVPAWEE----- 907
Db 618 IAA-----KCYFLRKAKAKQMPVMSRPVAPLLNSNNEKMSDPNMEANSHYHNDVVRNH 672
QY 908 -LQPVYTNANRGENVYSEVRIIOEKKHNAVADSPRLHNRKSGPILYSEVKVA 960
Db 673 AMKPINDNKEPLNSDVQYTEVQV-----SSAESHKDLGKDKTETVYSEVRKA 719
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RESULT 10
US-08-602-725-36
; Sequence 36, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DUBBIN, HELGA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-602-725-36
Query Match 6.2%; Score 316.5; DB 2; Length 698;
Best Local Similarity 19.5%; Pred. No. 2.8e-18;
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;
QY 29 PPWTVFQGERVTLCKGFRFSYQKTKWYHRYLKGKILRETPDNLILEVQE----- 79
Db 3 PPHRCIPQWRLTLTASLTLFWNPPTT-----AKLATIESTPFNVAEKGYLLLVHNL 55
QY 80 -----SGEY-----RCQAQGSPLSSPVHLDFSSASLILOAPLSVFEGD 117
Db 56 QHLFGYSWKYGERVDGNRQIIGVIGTQQTQATPGPAYSGREIYYPNASLLIQ----- 106
QY 118 SVVLRCAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPV 177
Db 107 -----NIIQND-----TGFVTLHVIKSDLVNEEATG----- 132
QY 178 SNTVKIQVQEPFTRPVLRASSQPTSG-NPVTLTCTQSLERSDVPFRFRDDQTLG 236
Db 133 ----QPRVYPELKPSPISNNKSPVEDKDAVFTCEPE----- 166
QY 237 LGWSLSFNPQITAMWSKDSGFYCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSPKA 296
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Db 167 -----TODATYLM-----WVNNQ-----SLPVSRLQ 188
Qy 297 LNFEGTKVTLHCETQEDSLRLYRFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCT 356
Db 189 LSNGRNLTLL-----FNVTRNDTASYKCE 212
Qy 357 ADNGLGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIF-EGAKVTLHCEAQRGSILYQPH 415
Db 213 TONPVSARRSDSVILNLYGPDAPTI---SPLNTSYRSGENLNLSCHA-ASNPPAQYSWF 268
Qy 416 ----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGPORSKAVSLSVTVV 470
Db 269 VNGTFQOSTQELFIPN-----ITVNSSGYTCQAHNSDGLNRTTITVIAEAP 318
Qy 471 SHPVLTLSSAEALTFEGATVTLHCEVGRSPQILYQFYHEDMPLW---SSSTPSVGRVSF 527
Db 319 PKPFIITSNNPNVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 367
Qy 528 S-----FSLTEGHSNGNYCTADNGFGPORSSEVSLFTV---PVSRLPILTLRPRA 575
Db 368 SNDNRTLTLSSVTRNDVGPYECGQNELSDVHSDPVLNLYGPDPTISPSVITYRPP-- 425
Qy 576 QAVVGDLELHCEAPRSGPILYFWFYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCE 635
Db 426 ----GVNLSLSCHAASNPPAQYSWLIDGNIQOHT-----QELFISNITEKNSGLYTCQ 474
Qy 636 ANGLVAOHSDDTISLSVIVPVSRLPILTFRAPRAQAVVG-DLLELHCEALRGSSPILYWFY 694
Db 475 ANNS-ASGHSRTTKTITVSAELPKPSISSNNKPKVEDKDAVFTCEPEAQNTTYLWVNN 533
Qy 695 HEDVTLGKISAPSGGASFNLSLITTEHSGIYSCDADNGLEAQRSEMVTILKAVPVSRLV 753
Db 534 GOSLPVSPRLQSLNGNRTTLFNVTRNDARAYVCGIQNSVSNRSDPVLNLYGPDPTI 593
Qy 754 LTRAPGTHAAVGDLELHCEALRGSPILYRFHEDVTLGNRSSPSGASLNSL----- 808
Db 594 IS--PPDSSYLSGANLNSCH-----SASNPSQVSWRINGIPIQ 631
Qy 809 -----LTABHSGNYSCEADNGLEAQRSETVTLITGLTANRSGPPFATGVAGGLLSI 859
Db 632 HTQVLFIAKITPNNGTYACFVSN-LATGRNNSIVKSIIVTSAGTSPGLSAGATVGM-- 688
Qy 860 AGLAAGALL 869
Db 689 IGVLVGVALI 698
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## RESULT 11

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US-09-949-016-6484
; Sequence 6484, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6484
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6484
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Query Match 6.28; Score 316.5; DB 4; Length 702;
Best Local Similarity 19.5%; Pred. No. 2.8e-18;
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;
Qy 29 PWTTFQGERVTLTCKGFRFYSPQTKWVHRVYLGKELRETDPNILEVOE----- 79
Db 7 PPHRWCIPIQRLLTASLLTFMNPPTT-----AKLTISTFNVAGKEVLLVNNLP 59
Qy 80 -----SGEY-----RCQAQGSPLSPVHLDFSSASLIIQAPLSVEGD 117
Db 60 QHLFGYSWKYGERVDGNRIIGVIGTQATPGPAYSGREIIYPNASLLIQ----- 110
Qy 118 SVVLCRAKAAEVLNNTIYKDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVS 177
Db 111 -----NIQND-----TGFYTLHVIKSLVNEEATG----- 136
Qy 178 SNTVKIQOVFPFPRVLRASSFOPISG-NPVTILTCTQLSLERSDVPRLRFRFRDDOTLG 236
Db 137 ----QRFVPELPKPSISSNNKPKVEDKDAVFTCEPE----- 170
Qy 237 LGWSLSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKA 296
Db 171 -----TQDATYLM-----WVNNQ-----SLPVSRLQ 192
Qy 297 LNFEGTKVTLHCETQEDSLRLYRFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCT 356
Db 193 LSNGRNLTLL-----FNVTRNDTASYKCE 216
Qy 357 ADNGLGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIF-EGAKVTLHCEAQRGSILYQPH 415
Db 217 TONPVSARRSDSVILNLYGPDAPTI---SPLNTSYRSGENLNLSCHA-ASNPPAQYSWF 272
Qy 416 ----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGPORSKAVSLSVTVV 470
Db 273 VNGTFQOSTQELFIPN-----ITVNSSGYTCQAHNSDGLNRTTITVIAEAP 322
Qy 471 SHPVLTLSSAEALTFEGATVTLHCEVGRSPQILYQFYHEDMPLW---SSSTPSVGRVSF 527
Db 323 PKPFIITSNNPNVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 371
Qy 528 S-----FSLTEGHSNGNYCTADNGFGPORSSEVSLFTV---PVSRLPILTLRPRA 575
Db 372 SNDNRTLTLSSVTRNDVGPYECGQNELSDVHSDPVLNLYGPDPTISPSVITYRPP-- 429
Qy 576 QAVVGDLELHCEAPRSGPILYFWFYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCE 635
Db 430 ----GVNLSLSCHAASNPPAQYSWLIDGNIQOHT-----QELFISNITEKNSGLYTCQ 478
Qy 636 ANGLVAOHSDDTISLSVIVPVSRLPILTFRAPRAQAVVG-DLLELHCEALRGSSPILYWFY 694
Db 479 ANNS-ASGHSRTTKTITVSAELPKPSISSNNKPKVEDKDAVFTCEPEAQNTTYLWVNN 537
Qy 695 HEDVTLGKISAPSGGASFNLSLITTEHSGIYSCDADNGLEAQRSEMVTILKAVPVSRLV 753
Db 538 GOSLPVSPRLQSLNGNRTTLFNVTRNDARAYVCGIQNSVSNRSDPVLNLYGPDPTI 597
Qy 754 LTRAPGTHAAVGDLELHCEALRGSPILYRFHEDVTLGNRSSPSGASLNSL----- 808
Db 598 IS--PPDSSYLSGANLNSCH-----SASNPSQVSWRINGIPIQ 635
Qy 809 -----LTABHSGNYSCEADNGLEAQRSETVTLITGLTANRSGPPFATGVAGGLLSI 859
Db 636 HTQVLFIAKITPNNGTYACFVSN-LATGRNNSIVKSIIVTSAGTSPGLSAGATVGM-- 692
Qy 860 AGLAAGALL 869
Db 693 IGVLVGVALI 702
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## RESULT 12

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US-08-389-459A-17
; Sequence 17, Application US/08389459A
; Patent No. 5817512
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us-09-724-254a-41.ra1

Thu May 5 15:11:00 2005

GENERAL INFORMATION:

APPLICANT: Morrow, Casey D. and Porter, Donna, C.  
 TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS  
 TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND  
 TITLE OF INVENTION: USING SAME  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 STATE STREET, SUITE 510  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/389,459A  
 FILING DATE: 15-FEB-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/087,009  
 FILING DATE: 01-JUL-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silveri, Jean M.  
 REGISTRATION NUMBER: 39,030  
 REFERENCE/DOCKET NUMBER: UAG-004CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 734 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-389-459A-17

Query Match 6.2%; Score 316.5; DB 2; Length 734;

Best Local Similarity 19.5%; Pred. No. 3e-18;  
 Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;

QY 29 PPWTTFQGRVTTCKGFRYSQKTKWYHLYGKELRETDPNILEVOE-----79  
 DB 39 PPHRCWCPQWRLLLTASLLTFWNPFTT-----AKLTISTPFWAEGREVLLLVHNL 91  
 QY 80 -----SGEY-----RCQAQGSPLSPVHLDFSSASLILOAPLSVPEGD 117  
 DB 92 QHLFGYSWYKGVGDGNQRIIGYVIGTQATPGAYSGREIIPNASLLIQ-----142  
 QY 118 SVVLCRAKAEVTLNNTIYKNDVLAFLNKTDPHIACKLKGNGAYRCTGYKESCCPV 177  
 DB 143 -----NIQND-----TGFTVLHVKSILVNEAATG-----168  
 QY 178 SNTVKIQVEPTTRPVLRASFPISG-NPVTLCETQLSLERSDVLPRFRFRDDQTLG 236  
 DB 169 -----QFRVVPFLPKPSISNNKPKVEDKDAVFTCEP-----202  
 QY 237 LGWSLSPNQITAMWKSQSGFYWCKAATPHSVISDSPRSWIQVQIPASHVPLTISPEKA 296  
 DB 203 -----TQDATYLM-----WVNNQ-----SLPVSPLRQ 224  
 QY 297 LNFEGTKVTLHCETOEDSLRILYRFHGVPLRHKSVCERGASFSPLTTNSGNYCT 356  
 DB 225 LSGNRTLT-----FNVTRNDTASYKCE 248  
 QY 357 ADNLGAKSKAVLSVTVFVSHVPLNLSPPEDLIF-EGAKVTLCEAQRGLSPILYQFH 415  
 DB 249 TQNPVSARRSDSVILNVLGPDAPTI---SPLNTSYRSGENLNLSCHA-ASNPAPQYSWF 304

QY 416 -----HEDAALERSANSAGGVAISFSLTAHSGNYCYCTADNG-FGPORSKAVSISITVPV 470  
 DB 305 VNGTQQSTQELFIEN-----ITVNSGSYTCQAHNSDTGLNRTTITVTVAEP 354  
 QY 471 SHPVLTLSSAEALTPEGATVTLHCEVQSGSPQILYQFHEMDPLW---SSSTPSVGRVSF 527  
 DB 355 PKPFTISNNSNVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQL 403  
 QY 528 S-----FSLTEHSGNYCYCTADNGFGPQSRSEVVSIFVTV---PVSRLPILTLRVPR 575  
 DB 404 SNDNRTLLSLVTRNDVGVYECIQNELSVDSHPVILNVLVGPDDPTISPSYTYRE-- 461  
 QY 576 QAVVGDLLEHCEAPRGSPPILYNFYHEDVTLGSSASPGGSEAFNLSLTAHSGNYSCE 635  
 DB 462 -----GVNLSLSCHAAASNPAPQYSLIDGNIQOHT-----QELFISNITEKNLSGLYTCQ 510  
 QY 636 ANGLVAQHSIDTISLIVPVSRLPILTFAPRAQAVVG-DLLEHCEALRGSSPLIYMFY 694  
 DB 511 ANNS-ASGHSRTTKTITVSALPKPISNNKPKVEDKDAVFTCEPEAQNTTYLWVN 569  
 QY 695 HEDVTGKISAPSGGASFNLSLTTTEHSGIYSCDADNGLEAQRSEMVTLKVAVPVSRPV 753  
 DB 570 GQSLPVSPLQLSNGNRTLTLENVTENDARAYVCGIQNSVSNRSDPVTLDVLYGPDTP 629  
 QY 754 LTLRAPGTHAAVGDLEHCEALRGSPILYRFFHEDVTLGNRSSPSGGASLNLS-----808  
 DB 630 IS--PPDSYLSGANLNLSC-----SASNPSPQYSWRINGIPOQ 667  
 QY 809 -----LTAHSGNYSCEADNGIACORSETVTIYITGLTANRSGPPATGVAGGLLSI 859  
 DB 668 HTQVLFIAKITPNNGTYACFVSN-LATGNNSIVKSITVSASCTSPGLSAGATVGIM-- 724  
 QY 860 AGLAAGALL 869  
 DB 725 IGLVGVALL 734

RESULT 13

US-08-987-867A-17  
 Sequence 17, Application US/08987867A  
 Patent No. 6063384

GENERAL INFORMATION:

APPLICANT: C. Morrow et al.  
 TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL  
 TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND  
 TITLE OF INVENTION: USING SAME  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 28 STATE STREET  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/987,867A  
 FILING DATE: 09-DEC-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/087,009  
 FILING DATE: 01-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Myers, Louis  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: UAP-004CPDV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214

;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
; LENGTH: 734 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-987-867A-17

Query Match 6.2%; Score 316.5; DB 3; Length 734;  
Best Local Similarity 19.5%; Pred. No. 3e-18;  
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;  
  
QY 29 PPWTTFQGERVLTCKGFRFPYSQKTKWHRYLKGLKILRETDPNILEVQE-----79  
Db 39 PPHRWCIQWRLLTASLLTFMNPPTT-----AKLTISTFPNVAEGKEVLLVHNLP 91  
QY 80 -----SGEY-----RCQAGSPLSSPVHLDFFSSASLILOAPLSVPEGD 117  
Db 92 QHLFGYSWYKGERVDGNRQIIGYVIGTQATPGPAYSGREIIPNASSLLIQ-----142  
QY 118 SVVLCRAKAEVLTNNIYKNDNVLAFLNKRDTDPHACLKONGAYRCTGYKESCCPVS 177  
Db 143 -----NIQND-----TGFTYTLHVKSIDLVAEEATG-----168  
QY 178 SNTVKIQVQEPFTRPVLRASSFPQISG-NPVTLTCTQSLERSDVPFRFRDDQTLG 236  
Db 169 -----QFRVPELPKPSISNNKPEVEDKDAVFTCEPE-----202  
QY 237 LGWSLSPNFQITAMWSKDSGFYWCCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKA 296  
Db 203 -----TQDATYLM-----WVNNQ-----SLPVSRLQ 224  
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCT 356  
Db 225 LSGNRTLT-----FNVTNRDTSYKCE 248  
QY 357 ADNGLGAKPSKAVLSVTVPVSHPVNLSSPEDLIP-EGAKVTLHCEAQRGSLPILYQFH 415  
Db 249 TQNPVSARRSDSVILNVLNYPDAPTI-----SPLNTSYRSGENLNLSCHA-ASNPPAQYSWF 304  
QY 416 -----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGQORSKAVLSITVPV 470  
Db 305 VNGTFQOSTQELFIPN-----ITVNSGSYTCQAHNSDTGLNRTVTITVYAE 354  
QY 471 SHPVLTLSSAEALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLW---SSSTPSVGRVSF 527  
Db 355 PKPFIITSNNSNPVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 403  
QY 528 S-----FSLTEGHSNGNYCTADNGFGQORSEVVSFLFTV-----PVSRLPILTLRVPRA 575  
Db 404 SNDNRTLTLSSVTRNDVGPYECGQNELSVDSHSDPVILNVLNYPDPTTISPSYTYRPP-- 461  
QY 576 QAVVGDLLEHCEAPRGSPILYWFYHEDVTLGSSNAPSCEASFNLSLTAHSGNYSC 635  
Db 462 -----GWNLSUSCHAAANPPAQYSLIDGNTQOHT-----QELFTSNITEKNSGLYTCQ 510  
QY 636 ANGLVAQHSDDTISLSVIVPVSRLPILTFAPRAQAVVG-DLLHLHCEALRGSSPILYWFY 694  
Db 511 ANNS-ASGSRRTVTKTIVTSAEALPKPSISNNKPEVEDKDAVFTCEPEAQNTYLLWVN 569  
QY 695 HEDVTLGKISAPGGGASFNL-SLTTEHSGIYSCADNGLGAEQRSEMTLKVAVPSRPV 753  
Db 570 GQSLPVSRLQSLNGNRTLTLFNVTNRDARAYCGIQNSVSNKSDPVTLDLVYGPDTPI 629  
QY 754 LTLRAPCTHAAGVDLLEHCEALRGSPILYRFFHEDVTLGNRSSPSGGASNLNS-----808  
Db 630 IS---PPDSSYLSGANLNSCH-----SASNPSQYSWRINGIPQ 667  
QY 809 -----LTASHSGNYSCADNGLGAEQRSEMTVTLYITGLTANRSGPFATGAGLLSI 859  
Db 668 HTQVLFIAKTPNNGTYACFVSN-LATGRNNSIVKSIIVSITVSAGTSFGLSAGATVGM-- 724  
QY 860 AGLAAGALLL 869

Db 725 IGVLVGVALI 734

## RESULT 14

US-09-949-016-8168  
; Sequence 8168, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8168  
; LENGTH: 740  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8168

Query Match 6.2%; Score 316.5; DB 4; Length 740;  
Best Local Similarity 19.5%; Pred. No. 3.1e-18;  
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;  
  
QY 29 PPWTTFQGERVLTCKGFRFPYSQKTKWHRYLKGLKILRETDPNILEVQE-----79  
Db 45 PPHRWCIQWRLLTASLLTFMNPPTT-----AKLTISTFPNVAEGKEVLLVHNLP 97  
QY 80 -----SGEY-----RCQAGSPLSSPVHLDFFSSASLILOAPLSVPEGD 117  
Db 98 QHLFGYSWYKGERVDGNRQIIGYVIGTQATPGPAYSGREIIPNASSLLIQ-----148  
QY 118 SVVLCRAKAEVLTNNIYKNDNVLAFLNKRDTDPHACLKONGAYRCTGYKESCCPVS 177  
Db 149 -----NIQND-----TGFTYTLHVKSIDLVAEEATG-----174  
QY 178 SNTVKIQVQEPFTRPVLRASSFPQISG-NPVTLTCTQSLERSDVPFRFRDDQTLG 236  
Db 175 -----QFRVPELPKPSISNNKPEVEDKDAVFTCEPE-----208  
QY 237 LGWSLSPNFQITAMWSKDSGFYWCCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKA 296  
Db 209 -----TQDATYLM-----WVNNQ-----SLPVSRLQ 230  
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCT 356  
Db 231 LSGNRTLT-----FNVTNRDTSYKCE 254  
QY 357 ADNGLGAKPSKAVLSVTVPVSHPVNLSSPEDLIP-EGAKVTLHCEAQRGSLPILYQFH 415  
Db 255 TQNPVSARRSDSVILNVLNYPDAPTI-----SPLNTSYRSGENLNLSCHA-ASNPPAQYSWF 310  
QY 416 -----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGQORSKAVLSITVPV 470  
Db 311 VNGTFQOSTQELFIPN-----ITVNSGSYTCQAHNSDTGLNRTVTITVYAE 360  
QY 471 SHPVLTLSSAEALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLW---SSSTPSVGRVSF 527  
Db 361 PKPFIITSNNSNPVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 409  
QY 528 S-----FSLTEGHSNGNYCTADNGFGQORSEVVSFLFTV-----PVSRLPILTLRVPRA 575  
Db 410 SNDNRTLTLSSVTRNDVGPYECGQNELSVDSHSDPVILNVLNYPDPTTISPSYTYRPP-- 467



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 103.659 Seconds  
(without alignments)  
3139.559 Million cell updates/sec

Title: US-09-724-254A-41  
Perfect score: 5116  
Sequence: 1 MLLWVILLVLPVSGQFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5116	100.0	977	14 US-10-040-862-10462	Sequence 10462, A
2	5116	100.0	977	15 US-10-057-475B-10462	Sequence 10462, A
3	5116	100.0	977	15 US-10-154-884B-10462	Sequence 10462, A
4	5116	100.0	977	15 US-10-403-847-9	Sequence 9, Appli
5	5116	100.0	977	16 US-10-764-324-10462	Sequence 10462, A
6	5104	99.8	977	14 US-10-241-220-97	Sequence 97, Appl
7	3923	76.7	759	15 US-10-040-862-10460	Sequence 10460, A
8	3923	76.7	759	15 US-10-057-475B-10460	Sequence 10460, A
9	3923	76.7	759	15 US-10-154-884B-10460	Sequence 10460, A
10	3923	76.7	759	15 US-10-403-847-7	Sequence 7, Appli
11	3923	76.7	759	16 US-10-764-324-10460	Sequence 10460, A
12	3897.5	76.2	790	15 US-10-403-847-4	Sequence 4, Appli
13	2962	57.9	592	14 US-10-040-862-10461	Sequence 10461, A

14 2962 57.9 592 15 US-10-057-475B-10461 Sequence 10461, A  
 15 2962 57.9 592 15 US-10-154-884B-10461 Sequence 10461, A  
 16 2962 57.9 592 15 US-10-403-847-8 Sequence 8, Appli  
 17 2962 57.9 592 16 US-10-764-324-10461 Sequence 10461, A  
 18 1854 36.2 438 15 US-10-403-847-6 Sequence 6, Appli  
 19 1559 30.5 707 15 US-10-108-260A-4774 Sequence 4774, Ap  
 20 1559 30.5 734 14 US-10-040-862-10463 Sequence 10463, A  
 21 1559 30.5 734 15 US-10-057-475B-10463 Sequence 10463, A  
 22 1559 30.5 734 15 US-10-154-884B-10463 Sequence 10463, A  
 23 1559 30.5 734 16 US-10-764-324-10463 Sequence 10463, A  
 24 1559 30.5 734 17 US-10-948-518-137 Sequence 137, App  
 25 1541.5 30.1 727 17 US-10-473-519-20 Sequence 20, Appli  
 26 1502 29.4 317 15 US-10-403-847-2 Sequence 2, Appli  
 27 1411 27.6 582 15 US-10-162-335-94 Sequence 94, Appl  
 28 1205.5 23.6 639 16 US-10-408-765A-2410 Sequence 2410, Ap  
 29 931.5 18.2 508 14 US-10-040-862-10464 Sequence 10464, A  
 30 931.5 18.2 508 15 US-10-057-475B-10464 Sequence 10464, A  
 31 931.5 18.2 508 15 US-10-154-884B-10464 Sequence 10464, A  
 32 931.5 18.2 508 15 US-10-154-884B-11039 Sequence 11039, A  
 33 931.5 18.2 508 16 US-10-764-324-10464 Sequence 10464, A  
 34 931.5 18.2 508 17 US-10-948-518-119 Sequence 119, App  
 35 900 17.6 181 16 US-10-363-829-286 Sequence 286, App  
 36 900 17.6 181 16 US-10-363-829-431 Sequence 431, App  
 37 884.5 17.3 327 15 US-10-363-616-458 Sequence 458, App  
 38 871.5 17.0 421 15 US-10-162-335-96 Sequence 96, Appl  
 39 871.5 17.0 421 15 US-10-162-335-98 Sequence 11043, A  
 40 864.5 16.9 445 15 US-10-154-884B-11043 Sequence 11048, A  
 41 861 16.8 460 15 US-10-154-884B-11048 Sequence 11048, A  
 42 851.5 16.6 421 15 US-10-162-335-100 Sequence 100, App  
 43 826.5 16.2 515 14 US-10-040-862-10459 Sequence 10459, A  
 44 826.5 16.2 515 15 US-10-057-475B-10459 Sequence 10459, A  
 45 826.5 16.2 515 15 US-10-154-884B-10459 Sequence 10459, A

#### ALIGNMENTS

#### RESULT 1

US-10-040-862-10462  
 ; Sequence 10462, Application US/10040862  
 ; Publication No. US20030078396A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Corixa Corporation  
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ; TITLE OF INVENTION: Hematological Malignancies  
 ; FILE REFERENCE: 014058-013520US  
 ; CURRENT APPLICATION NUMBER: US/10/040,862  
 ; CURRENT FILING DATE: 2001-11-06  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/186,126  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/190,479  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200,545  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: US 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: US 60/223,416

841 TANRSGPATGVAGGLISLGIAGLALCYLWLSKAGRKAPSPARSPSDSDSQEPTYH 900  
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901 NVPAMEELQPVYTNANPRGENVYSEVR11QEKKHAVASDPRLHKNKGSPIIYSEKVA 960  
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RESULT 2

US-10-057-475B-10462  
; Sequence 10462, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10462  
; LENGTH: 977  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-057-475B-10462

Query Match 100.0%; Score 5116; DB 15; Length 977;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120

; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10462  
; LENGTH: 977  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-040-862-10462

Query Match 100.0%; Score 5116; DB 14; Length 977;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSQKTKWYHR 60  
Db 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSQKTKWYHR 60  
Qy 61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120  
Db 61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKNDGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQPFTRPVLRASSFOPISGNPVTLTCETQLSRLSDVPLRFRFRDQTLGLGWS 240  
Db 181 VKIQVQPFTRPVLRASSFOPISGNPVTLTCETQLSRLSDVPLRFRFRDQTLGLGWS 240  
Qy 241 LSPNFQITAMWSDGSGFYKCAATMPSHVISDSRSMQVQIPASHPVLTLSPEKALNE 300  
Db 241 LSPNFQITAMWSDGSGFYKCAATMPSHVISDSRSMQVQIPASHPVLTLSPEKALNE 300  
Qy 301 GTKVTLHCETQEDSLRTLYRHYEGVPLRHKSVRCERGAISFSLTENGNYICTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLYRHYEGVPLRHKSVRCERGAISFSLTENGNYICTADNG 360  
Qy 361 LGAKPSKAVSLSVTVVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPIYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTVVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPIYQFHEDAA 420  
Qy 421 LERRSANGAGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTVVSHPVNLSSA 480  
Db 421 LERRSANGAGVAISFSLTAHSGNYICTADNGFGPQRSKAVSLSVTVVSHPVNLSSA 480  
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPSVGRVSPFSITGHSNYY 540  
Db 481 EALTPEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPSVGRVSPFSITGHSNYY 540  
Qy 541 CTADNGFGQRSEVSVLFTVTVPSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600  
Db 541 CTADNGFGQRSEVSVLFTVTVPSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600  
Qy 601 YHEDVTLGSSAPSGEASFNLSTAHSNGYSCANNGLVAQHSDDTISLSVIVPSRPI 660  
Db 601 YHEDVTLGSSAPSGEASFNLSTAHSNGYSCANNGLVAQHSDDTISLSVIVPSRPI 660  
Qy 661 LTRAPRAQAVGDLLEHCEALRGSSPLTYFYHEDVTGKISAPSGGASFNLSLTFE 720  
Db 661 LTRAPRAQAVGDLLEHCEALRGSSPLTYFYHEDVTGKISAPSGGASFNLSLTFE 720  
Qy 721 HSGIYSCADNGLGAQRSEMTLKVAVPSRPIVTLRAPGTHAAVGDLEHCEALRGSP 780  
Db 721 HSGIYSCADNGLGAQRSEMTLKVAVPSRPIVTLRAPGTHAAVGDLEHCEALRGSP 780  
Qy 781 LILYRPFHEDVTGNSPSSGGASLNLSTAHSNGYSCADNGLGAQRSETVTLTYTGL 840  
Db 781 LILYRPFHEDVTGNSPSSGGASLNLSTAHSNGYSCADNGLGAQRSETVTLTYTGL 840

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QY 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRTDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRTDHPHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCEQEDSLRTLYRFGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTILHCEQEDSLRTLYRFGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540
Db 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540
QY 541 CTADNGFGPQSEVSVLFTVTVPSRPILTILRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQSEVSVLFTVTVPSRPILTILRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTRAPPAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db 661 LTRAPPAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
QY 721 HSGIYSCADNGLAEQSEMVTLKVAVPVSRPVLTLRAPGTHAAVGLLEHCEALRGSP 780
Db 721 HSGIYSCADNGLAEQSEMVTLKVAVPVSRPVLTLRAPGTHAAVGLLEHCEALRGSP 780
QY 781 LILYRPFHEDVTLGNRSSPGGASLNLSTLAHSGNYSCEADNGLGQQRSETVLYITGL 840
Db 781 LILYRPFHEDVTLGNRSSPGGASLNLSTLAHSGNYSCEADNGLGQQRSETVLYITGL 840
QY 841 TANRSGPFATGVAGLLSIAAGALLLYCWLSRKAGRPASDPARSPSDSDSQEPTYH 900
Db 841 TANRSGPFATGVAGLLSIAAGALLLYCWLSRKAGRPASDPARSPSDSDSQEPTYH 900
QY 901 NVPAWELQPYTNANPRGENVYSEVRIIOEKKKHAVAADPRHLRNKGSPIIYSEVKVA 960
Db 901 NVPAWELQPYTNANPRGENVYSEVRIIOEKKKHAVAADPRHLRNKGSPIIYSEVKVA 960
QY 961 STPVGSLFLASSAPHR 977
Db 961 STPVGSLFLASSAPHR 977
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## RESULT 3

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US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
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; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10462
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Query Match 100.0%; Score 5116; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVLAPVGGFQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFVSPQTKWYHR 60
Db 1 MLLWVILLVLAPVGGFQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFVSPQTKWYHR 60
QY 61 YLCKEILRETPDNILEVQESGEVRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
Db 61 YLCKEILRETPDNILEVQESGEVRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
QY 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRTDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRTDHPHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCEQEDSLRTLYRFGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTILHCEQEDSLRTLYRFGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540
Db 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540
QY 541 CTADNGFGPQSEVSVLFTVTVPSRPILTILRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
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Db	541	CTADNGFGQSRSEVSLFVTVPSRPILTLAVPRAQAVVGDLELHCEAPRGSPPILYWF	600
Qy	601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAOHSDDTISLVIIPVSRPI	660
Db	601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAOHSDDTISLVIIPVSRPI	660
Qy	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE	720
Db	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE	720
Qy	721	HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILTLAPGTHAAVGDLELHCEALRGSP	780
Db	721	HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILTLAPGTHAAVGDLELHCEALRGSP	780
Qy	781	LILYRFHEDVTLGNRSSPGASNLSTAHSGNYSCEADNGIAGORSETVLIYITGL	840
Db	781	LILYRFHEDVTLGNRSSPGASNLSTAHSGNYSCEADNGIAGORSETVLIYITGL	840
Qy	841	TANRSGPFATGVAGGLSLTAGLAAGALLLYCWLRSKAGRKPADSPARSPSDSQEPTIYH	900
Db	841	TANRSGPFATGVAGGLSLTAGLAAGALLLYCWLRSKAGRKPADSPARSPSDSQEPTIYH	900
Qy	901	NVPAMELOQVYTNANPRGENVYSEVRIIQEKKHAVASDPRHLRNGKSPPIIYSEVKVA	960
Db	901	NVPAMELOQVYTNANPRGENVYSEVRIIQEKKHAVASDPRHLRNGKSPPIIYSEVKVA	960
Qy	961	STPVSGSLFLASSAPHR	977
Db	961	STPVSGSLFLASSAPHR	977

RESULT 4

US-10-403-847-9

; Sequence 9, Application US/10403847

; Publication No. US20040030098A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN

; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGSSG AND BGSSG

; FILE REFERENCE: D0228 NP

; CURRENT APPLICATION NUMBER: US/10/403,847

; CURRENT FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: U.S. 60/368,671

; PRIOR FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: U.S. 60/371,420

; PRIOR FILING DATE: 2002-04-10

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 9

; LENGTH: 977

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-403-847-9

Query Match	100.08;	Score	5116;	DB	15;	Length	977;
Best Local Similarity	100.08;	Pred. No.	0;				
Matches	977;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

Qy	1	MLLWILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR	60
Db	1	MLLWILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR	60
Qy	61	YLKGRILRETPNILEVQESGYRQAGQSPSSPHVLDFFSSALILQAPLVSVEGDSV	120
Db	61	YLKGRILRETPNILEVQESGYRQAGQSPSSPHVLDFFSSALILQAPLVSVEGDSV	120
Qy	121	LRCAKAEVTLNNTIYKNDVLAFLNKRTHFPHACLKNGAYRGTCTYKESCCPVSSNT	180
Db	121	LRCAKAEVTLNNTIYKNDVLAFLNKRTHFPHACLKNGAYRGTCTYKESCCPVSSNT	180
Qy	181	VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQSLERSDVPLRFRFRDDQTILGLWS	240

Db	181	VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQSLERSDVPLRFRFRDDQTILGLWS	240
Qy	241	LSPNFQITAMWKSDFYCKAATMPHSVISDSRPSWQIQVQIPASHPVLTLSPEKALNFE	300
Db	241	LSPNFQITAMWKSDFYCKAATMPHSVISDSRPSWQIQVQIPASHPVLTLSPEKALNFE	300
Qy	301	GTKVTILHCEQEDSLRTLYRFVHEGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG	360
Db	301	GTKVTILHCEQEDSLRTLYRFVHEGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG	360
Qy	361	LGAKPSKAVSLSVTVPSVHPVNLNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420
Db	361	LGAKPSKAVSLSVTVPSVHPVNLNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420
Qy	421	LERRSANSAGGVAISFSLTAHSGNYSCTADNGFGPQRSKAVSLSTITVPSHPVLTLSA	480
Db	421	LERRSANSAGGVAISFSLTAHSGNYSCTADNGFGPQRSKAVSLSTITVPSHPVLTLSA	480
Qy	481	EALTFFEGATVTLHCEVQGRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
Db	481	EALTFFEGATVTLHCEVQGRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY	540
Qy	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRQAQAVVGDLELHCEAPRGSPPILYWF	600
Db	541	CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRQAQAVVGDLELHCEAPRGSPPILYWF	600
Qy	601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAOHSDDTISLVIIPVSRPI	660
Db	601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAOHSDDTISLVIIPVSRPI	660
Qy	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE	720
Db	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE	720
Qy	721	HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILTLAPGTHAAVGDLELHCEALRGSP	780
Db	721	HSGIYSCDADNGLEAQRSEMTLVKAVPVSRPILTLAPGTHAAVGDLELHCEALRGSP	780
Qy	781	LILYRFHEDVTLGNRSSPGASNLSTAHSGNYSCEADNGIAGORSETVLIYITGL	840
Db	781	LILYRFHEDVTLGNRSSPGASNLSTAHSGNYSCEADNGIAGORSETVLIYITGL	840
Qy	841	TANRSGPFATGVAGGLSLTAGLAAGALLLYCWLRSKAGRKPADSPARSPSDSQEPTIYH	900
Db	841	TANRSGPFATGVAGGLSLTAGLAAGALLLYCWLRSKAGRKPADSPARSPSDSQEPTIYH	900
Qy	901	NVPAMELOQVYTNANPRGENVYSEVRIIQEKKHAVASDPRHLRNGKSPPIIYSEVKVA	960
Db	901	NVPAMELOQVYTNANPRGENVYSEVRIIQEKKHAVASDPRHLRNGKSPPIIYSEVKVA	960
Qy	961	STPVSGSLFLASSAPHR	977
Db	961	STPVSGSLFLASSAPHR	977

RESULT 5

US-10-764-324-10462

; Sequence 10462, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126



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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10462

Query Match      100.0%; Score 5116; DB 16; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
QY 241 LSPNFQITAMWSKDSGYWCCKAATMPSHVSIDSRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCCKAATMPSHVSIDSRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTRVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCTADNG 360
DB 301 GTRVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLVTPVSHVPLNLSGPDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLVTPVSHVPLNLSGPDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHVPLTSSA 480
DB 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHVPLTSSA 480
QY 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSPSLTGHSGNYY 540
DB 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSPSLTGHSGNYY 540
QY 541 CTADNGFGPQRSVSLFVTVPVSRPILTLRVRAQAVVGDLLHCEAPRGSPFPILYWF 600
DB 541 CTADNGFGPQRSVSLFVTVPVSRPILTLRVRAQAVVGDLLHCEAPRGSPFPILYWF 600
QY 601 YHEDVTLGSSASPGGEASFNLSLTAHSGNYSCEANNGLVLAOHSOTISLSVIVPVSRI 660
DB 601 YHEDVTLGSSASPGGEASFNLSLTAHSGNYSCEANNGLVLAOHSOTISLSVIVPVSRI 660

661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
721 HSGIYSCDADNGLEAQRSEWVTLKVAVPVSRPVLTLRAPGTHAAVGDLLHCEALRGSP 780
721 HSGIYSCDADNGLEAQRSEWVTLKVAVPVSRPVLTLRAPGTHAAVGDLLHCEALRGSP 780
781 LILYRPFHEDVTILGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGARQSETVLYITGL 840
781 LILYRPFHEDVTILGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGARQSETVLYITGL 840
841 TANRSGPFATGVAGGLSLTAGLAAGALLYLWLSRKAGRKPAADPARSPSDSDSQEPTYH 900
841 TANRSGPFATGVAGGLSLTAGLAAGALLYLWLSRKAGRKPAADPARSPSDSDSQEPTYH 900
901 NVPAMEELQPVYTNANPRGENVYSEVRITIQEKKHAAVADPRHLRNKGSPIIYSEVKVA 960
901 NVPAMEELQPVYTNANPRGENVYSEVRITIQEKKHAAVADPRHLRNKGSPIIYSEVKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 6
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US200301048408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: F5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

Query Match      99.8%; Score 5104; DB 14; Length 977;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
QY 241 LSPNFQITAMWSKDSGYWCCKAATMPSHVSIDSRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCCKAATMPSHVSIDSRSWIOVQIPASHPVLTLSPEKALNFE 300
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Thu May 5 15:11:00 2005

us-09-724-254a-41.rapb

241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300  
301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360  
301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360  
361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHEDAA 420  
361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHEDAA 420  
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480  
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480  
481 EALTPEGATVTLHCEVQRGSPQILYQFHEDMPLSSSTPSVGRVSFSLTEGHSNGNY 540  
481 EALTPEGATVTLHCEVQRGSPQILYQFHEDMPLSSSTPSVGRVSFSLTEGHSNGNY 540  
541 CTADNGFGQPSKAVSLSVTPVSRPILTLRVPRAQAVVGDILLEHCEAPRGSPLILYWF 600  
541 CTADNGFGQPSKAVSLSVTPVSRPILTLRVPRAQAVVGDILLEHCEAPRGSPLILYWF 600  
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660  
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660  
661 LTRPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720  
661 LTRPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720  
721 HSGIYSCADNGLEAQRSEMTUKVAVPSRPLTLRAGTHAAVGDILLEHCEALRGSP 780  
721 HSGIYSCADNGLEAQRSEMTUKVAVPSRPLTLRAGTHAAVGDILLEHCEALRGSP 780  
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAEHSNYSCEANGLGAQORSETVTLITGL 840  
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAEHSNYSCEANGLGAQORSETVTLITGL 840  
841 TANRSGPFATGVAGGLSLIAGLALLYCWLSRAGKRPASDPARSDDSDSQEPTVH 900  
841 TANRSGPFATGVAGGLSLIAGLALLYCWLSRAGKRPASDPARSDDSDSQEPTVH 900  
901 NVPWELQPVYTNANRGENVYSEVRILQEKKHAVASDPRLHKNKGSPIIYSEVKVA 960  
901 NVPWELQPVYTNANRGENVYSEVRILQEKKHAVASDPRLHKNKGSPIIYSEVKVA 960  
961 STPVSGSLFLASSAPHR 977  
961 STPVSGSLFLASSAPHR 977

RESULT 7  
US-10-040-862-10460  
; Sequence 10460, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies.  
; FILE REFERENCE: 014058-0135200S  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 09/796,692  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10460  
LENGTH: 759  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-040-862-10460

Query Match 76.7%; Score 3923; DB 14; Length 759;  
Best Local Similarity 100.0%; Pred. No. 7.6e-266;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGPRFSPQTKWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGPRFSPQTKWYHR 60  
QY 61 YLGEILLRETPDNLTEVQESGEYRCQAGSPVHLDPFSSASLIQAPLSVFEGSVV 120  
DB 61 YLGEILLRETPDNLTEVQESGEYRCQAGSPVHLDPFSSASLIQAPLSVFEGSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHPIACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHPIACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCETOLSLERSDPLRFRFRDDQTLGLGWS 240  
DB 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCETOLSLERSDPLRFRFRDDQTLGLGWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360  
DB 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480  
QY 481 EALTPEGATVTLHCEVQRGSPQILYQFHEDMPLSSSTPSVGRVSFSLTEGHSNGNY 540  
DB 481 EALTPEGATVTLHCEVQRGSPQILYQFHEDMPLSSSTPSVGRVSFSLTEGHSNGNY 540  
QY 541 CTADNGFGQPSKAVSLSVTPVSRPILTLRVPRAQAVVGDILLEHCEAPRGSPLILYWF 600  
DB 541 CTADNGFGQPSKAVSLSVTPVSRPILTLRVPRAQAVVGDILLEHCEAPRGSPLILYWF 600  
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660  
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660

Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660  
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Qy 721 HSGIYSCEADNGLEAQRSEMWTLKVA 746  
Db 721 HSGIYSCEADNGLEAQRSEMWTLKVA 746

RESULT 8  
US-10-057-475B-10460  
; Sequence 10460, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 10460  
; LENGTH: 759  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-057-475B-10460

Query Match 76.7%; Score 3923; DB 15; Length 759;  
Best Local Similarity 100.0%; Pred. No. 7.6e-266;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60  
Qy 61 YLGEKILRETFDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLIIQAPLSVFGDSVV 120  
Db 61 YLGEKILRETFDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLIIQAPLSVFGDSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRQTDPHI PHACLKDNKGAYRCTGYKESCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRQTDPHI PHACLKDNKGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCTETQLSLERSDVPILRFRFFRDDDTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCTETQLSLERSDVPILRFRFFRDDDTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPKALNPE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPKALNPE 300  
Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTSTENGNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTSTENGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIIFGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIIFGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Qy 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVPSHPVLTLSSA 480  
Db 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVPSHPVLTLSSA 480  
Qy 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTSGHSGNY 540  
Db 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTSGHSGNY 540  
Qy 541 CTADNGFGPQRSVWSLFTVPSRPIILTVRPAQAVVGDLLHCEAQRGSPPILYWF 600  
Db 541 CTADNGFGPQRSVWSLFTVPSRPIILTVRPAQAVVGDLLHCEAQRGSPPILYWF 600  
Qy 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660  
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660  
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Qy 721 HSGIYSCEADNGLEAQRSEMWTLKVA 746  
Db 721 HSGIYSCEADNGLEAQRSEMWTLKVA 746

RESULT 9  
US-10-154-884B-10460  
; Sequence 10460, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154,884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201

Thu May 5 15:11:00 2005

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

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Query Match          76.7%; Score 3923; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60
QY 61 YLQKEILRETPDNILVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120
DB 61 YLQKEILRETPDNILVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDDTGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDDTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMHSVSDSPRSWIVQIIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMHSVSDSPRSWIVQIIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSSA 480
QY 481 EALTPEGATVTLHCEVQQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTPEGATVTLHCEVQQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGPQRSSEVSVLFTVPSRPIILTRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSSEVSVLFTVPSRPIILTRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
DB 661 LTRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
QY 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746
DB 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746

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RESULT 10  
US-10-403-847-7

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; Sequence 7, Application US/10403847
; Publication NO. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
; CELL SURFACE PROTEIN WITH IMMUNOLOGOBULIN FOLDS, BGS5G AND BGS51
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

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Query Match          76.7%; Score 3923; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60
QY 61 YLQKEILRETPDNILVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120
DB 61 YLQKEILRETPDNILVQESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDDTGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCETQLSLERSDVLPRFRFRDDDTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMHSVSDSPRSWIVQIIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMHSVSDSPRSWIVQIIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSSA 480
QY 481 EALTPEGATVTLHCEVQQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTPEGATVTLHCEVQQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGPQRSSEVSVLFTVPSRPIILTRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSSEVSVLFTVPSRPIILTRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
DB 661 LTRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720

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Qy 721 HSGIYSCADNGLEAQRSEMTLKV 746  
Db 721 HSGIYSCADNGLEAQRSEMTLKV 746

RESULT 11  
US-10-764-324-10460  
; Sequence 10460, Application US/10764324  
; Publication No. US20040175739A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/764,324  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US/10/040,862  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10460  
; LENGTH: 759  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-764-324-10460

Query Match 76.7%; Score 3923; DB 16; Length 759;  
Best Local Similarity 100.0%; Pred. No. 7.6e-266;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60

Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQDSVV 120  
Db 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVEPFRTPVLRASSFQIPISGNPVTLTCTETQLSLERSDVLFRFRDDOTLGLGWS 240  
Db 181 VKIQVEPFRTPVLRASSFQIPISGNPVTLTCTETQLSLERSDVLFRFRDDOTLGLGWS 240

Qy 241 LSNFQITAMWSKDSGYWCKAATMPSHVLSDSRWSIQVQIPASHPVLTLSPEKALNPE 300  
Db 241 LSNFQITAMWSKDSGYWCKAATMPSHVLSDSRWSIQVQIPASHPVLTLSPEKALNPE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTTENGSGNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTTENGSGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 EALTTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
Db 481 EALTTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy 541 CTADNGFGPORSEVSLFVTVPSRPLTLRVPRQAQVGDLLHCEAQRGSPPILYWF 600  
Db 541 CTADNGFGPORSEVSLFVTVPSRPLTLRVPRQAQVGDLLHCEAQRGSPPILYWF 600

Qy 601 YHEDVTLGSSSAPSGGEASFNLSTAEHSGNYSCAANNGLVAQHSDTISLSVIVPVSRIPI 660  
Db 601 YHEDVTLGSSSAPSGGEASFNLSTAEHSGNYSCAANNGLVAQHSDTISLSVIVPVSRIPI 660

Qy 661 LTPRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Db 661 LTPRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720

Qy 721 HSGIYSCADNGLEAQRSEMTLKV 746  
Db 721 HSGIYSCADNGLEAQRSEMTLKV 746

RESULT 12  
US-10-403-847-4  
; Sequence 4, Application US/10403847  
; Publication No. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICER VARIANTS OF A HUMAN  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403,847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371,420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-847-4

Query Match 76.2%; Score 3897.5; DB 15; Length 790;  
Best Local Similarity 96.0%; Pred. No. 4.9e-264;  
Matches 746; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60

Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQDSVV 102  
Db 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQDSVV 102

Qy 103 -----ASLILQAPLSVFEQDSVVLRCAKAEVTLNNTIYKNDNVLAFLNKR 149  
Db 121 DLTWASQAGITASLILQAPLSVFEQDSVVLRCAKAEVTLNNTIYKNDNVLAFLNKR 180

Qy 150 DFHIFACLDKNGAYRCTGYKESCCPVSSNTVKIQVEPFRTPVLRASSFQIPISGNPVTL 209

Thu May 5 15:11:00 2005

181 DBFHIPACIKONGAYRCTGYKESCCPVSSNTVKIQVEPFRPVRASSFQPSGNEPVT 240  
210 TCETOLSLERSDVLPRFFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSV 269  
241 TCETOLSLERSDVLPRFFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSV 300  
270 ISDSPRSMTQVQIPASHVPLTSPKALNPFEGTKVTLHCETOEDSLRLTYRFYHEGVPLR 329  
301 ISDSPRSMTQVQIPASHVPLTSPKALNPFEGTKVTLHCETOEDSLRLTYRFYHEGVPLR 360  
330 HKSVCRCGASISFSLTTENSNGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPED 389  
361 HKSVCRCGASISFSLTTENSNGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPED 420  
390 LIPEGAKVTLHCEAQRGSILPILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCYT 449  
421 LIPEGAKVTLHCEAQRGSILPILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCYT 480  
450 ADNGRGPORSKAVSLSVTPVSHVPLTSSAALTFEGATVTLHCEVQSGSPQILYQFYH 509  
481 ADNGRGPORSKAVSLSVTPVSHVPLTSSAALTFEGATVTLHCEVQSGSPQILYQFYH 540  
510 EDMPLWSSSTPVSRYGVSFSLTEHSGNYCYTADNGFGPQSEVVSILFVTPVSRPILT 569  
541 EDMPLWSSSTPVSRYGVSFSLTEHSGNYCYTADNGFGPQSEVVSILFVTPVSRPILT 600  
570 LRVPRQAQVGDLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGEASFNLSTAHS 629  
601 LRVPRQAQVGDLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGEASFNLSTAHS 660  
630 GNYSCAANGLVAQHSITISLIVPVSREPILTFRAPRAQVAGDLELHCEALRGSSPI 689  
661 GNYSCAANGLVAQHSITISLIVPVSREPILTFRAPRAQVAGDLELHCEALRGSSPI 720  
690 LYWFYHEDVTLGKISAPSGGASPNLSLTTEHSGIYSCADNGLEAQRSEMTLKVA 746  
721 LYWFYHEDVTLGKISAPSGGASPNLSLTTEHSGIYSCADNGLEAQRSEMTLKVA 777

RESULT 13  
US-10-040-862-10461  
; Sequence 10461, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: US 60/223,416  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/223,378  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 09/796,692  
PRIOR FILING DATE: 2001-03-01  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 10461  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-040-862-10461  
Query Match 57.9%; Score 2962; DB 14; Length 592;  
Best Local Similarity 98.6%; Pred. No. 1.1e-198; Indels 4; Gaps 1;  
Matches 564; Conservative 0; Mismatches 4  
QY 1 MLLWVILLVLAPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60  
DB 1 MLLWVILLVLAPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQTKWYHR 60  
QY 61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSVV 120  
QY 121 LRCAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIPHACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIPHACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVQPPFTRPVLRASSFPISGNPVTLCETQLSLERSDVLPRFRFDDOTLGLWS 240  
DB 181 VKIQVQPPFTRPVLRASSFPISGNPVTLCETQLSLERSDVLPRFRFDDOTLGLWS 240  
QY 241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHVPLTSPKALNFE 300  
DB 241 LSPNQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHVPLTSPKALNFE 300  
QY 301 GTKVTLHCETOEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
DB 301 GTKVTLHCETOEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSILPILYQPHHEDA 420  
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSILPILYQPHHEDA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPQSKAVSLSVTPVSHVPLTSSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPQSKAVSLSVTPVSHVPLTSSA 480  
QY 481 EALTPEGATVTLHCEVQSGSPQILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCY 540  
DB 481 EALTPEGATVTLHCEVQSGSPQILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCY 540  
QY 541 CTADNGFGPQSEVVSILFVT---VPSGRPIL 568  
DB 541 CTADNGFGPQSEVVSILFVTGKCVLASHPPL 572

RESULT 14  
US-10-057-475B-10461  
; Sequence 10461, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
FILE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-014402US  
CURRENT APPLICATION NUMBER: US/10/057,475B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10979  
SOFTWARE: Fast-Seq for Windows Version 3.0  
SEQ ID NO 10461  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-057-475B-10461

Query Match 57.9%; Score 2962; DB 15; Length 592;  
Best Local Similarity 98.6%; Pred. No. 1.1e-198;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60  
Qy 61 YLGEKILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120  
Db 61 YLGEKILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Qy 301 GTKVTLHCETQBSLRTLRYFYHGVPLRHKSVRCERGAISFSLTTENSGNYCTADNG 360  
Db 301 GTKVTLHCETQBSLRTLRYFYHGVPLRHKSVRCERGAISFSLTTENSGNYCTADNG 360  
Qy 361 LGAKPSKAVSLVTPVSHVNLSSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420  
Db 361 LGAKPSKAVSLVTPVSHVNLSSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420  
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSIITVPVSHPVLTLSA 480  
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSIITVPVSHPVLTLSA 480  
Qy 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Db 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
Qy 541 CTADNGFGPORSVSVSLFVT---VPVSRPIL 568  
Db 541 CTADNGFGPORSVSVSLFVTGKCVLASHPPL 572  
RESULT 15  
US-10-154-884B-10461  
Sequence 10461, Application US/10154884B  
Publication No. US20040005561A1  
GENERAL INFORMATION:  
APPLICANT: Gaigert, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Retter, Marc W.  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
FILE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-013521US  
CURRENT APPLICATION NUMBER: US/10/154,884B  
CURRENT FILING DATE: 2002-05-23  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 11290  
SOFTWARE: Fast-Seq for Windows Version 3.0  
SEQ ID NO 10461  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-154-884B-10461

Query Match 57.9%; Score 2962; DB 15; Length 592;  
Best Local Similarity 98.6%; Pred. No. 1.1e-198;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60  
Qy 61 YLGEKILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120  
Db 61 YLGEKILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCTQLSLERSDVPFRFRDDOTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300



Thu May 5 15:11:00 2005

Db	241	LSFNFIITAMWSKDSGFIWCKAATPHSVISDSPRSNIQVOIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRRCERGASISFSLTTTENSNGNYCTADNG	360
Db	301	GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRRCERGASISFSLTTTENSNGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
Db	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA	480
Db	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA	480
QY	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEHSGNYY	540
Db	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEHSGNYY	540
QY	541	CTADNGFGPQRSEVWSLFTVTVVSVSRPIL	568
Db	541	CTADNGFGPQRSEVWSLFTVTVVSVSRPIL	572

Search completed: May 4, 2005, 12:01:18  
Job time : 106.659 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:24:30 ; Search time 30.6362 Seconds  
(without alignments)  
3068.392 Million cell updates/sec

Title: US-09-724-254A-41  
Perfect score: 5116  
Sequence: 1 MLHWVILLVLPVSGQFART.....KVASTVPVSGSLFIASSAPHR 977

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545.5	10.7	255	2 JC7593	SH2 domain-contain
2	418.5	8.2	344	2 A41357	Pc gamma (IgG) rec
3	418.5	8.2	374	1 A39878	Pc gamma (IgG) rec
4	412	8.1	4351	2 A38096	perlecan precursor
5	402.5	7.9	404	2 A46480	Pc gamma (IgG) rec
6	396	7.7	336	2 I48471	Pc gamma (IgG) rec
7	396	7.7	7962	2 I38346	elastic titin - hu
8	361	7.1	3707	2 S18252	heparan sulfate pr
9	351.5	6.9	738	2 A40096	platelet-endotheli
10	333.5	6.5	847	2 JH0371	B-cell adhesion pr
11	331	6.5	5175	2 T20992	hypothetical prote
12	331	6.5	5198	2 T43290	hemiscitin precurs
13	330	6.5	862	2 I49583	differentiation an
14	330	6.5	1327	2 T09402	immunoglobulin-lik
15	327	6.4	1634	2 S50065	sialoadhesin - mou
16	326.5	6.4	2396	2 I46021	Pc-gamma receptor
17	326	6.4	1896	2 T08851	Down syndrome cell
18	324	6.3	4162	2 T42633	connectin/titin -
19	319	6.2	270	2 A34636	Pc-gamma receptor
20	316.5	6.2	702	2 A36319	carcinoembryonic a
21	312	6.1	868	2 A46512	CD22 homoloy/B lym
22	292.5	5.7	254	1 JLO107	Pc gamma (IgG) rec
23	292	5.7	223	1 JU0284	Pc gamma (IgG) rec
24	290	5.7	323	2 S06946	Pc gamma (IgG) rec
25	289	5.6	310	2 JLO119	Pc gamma (IgG) rec
26	287.5	5.6	1070	2 JC4593	protein-tyrosine k
27	286	5.6	3375	2 T19821	hypothetical prote
28	285.5	5.6	1323	2 PN0568	connectin 3B - chi
29	284	5.6	1051	2 A39712	kinase-like protei

30	281	5.5	917	2 I48950	telencephalin prec
31	267	5.2	257	2 S00682	IgE Fc receptor al
32	266	5.2	1256	2 T03096	CDO protein - rat
33	265.5	5.2	1240	2 T03097	CDO protein - huma
34	264.5	5.2	317	2 JLO118	Pc gamma (IgG) rec
35	262	5.1	285	2 S36903	Pc gamma (IgG) rec
36	259	5.1	6642	2 T29757	protein UNC-89 - C
37	257	5.0	261	2 S29360	Pc gamma (IgG) rec
38	256	5.0	280	2 I55577	Pc gamma (IgG) rec
39	253.5	5.0	283	1 FCMSG1	Pc gamma (IgG) rec
40	253.5	5.0	330	2 A40071	Pc gamma (IgG) rec
41	253.5	5.0	330	2 I49660	Pc gamma-1/gamma-2
42	252	4.9	1651	2 T14160	transmembrane rece
43	251	4.9	1091	1 IJCHNL	neural cell adhesi
44	251	4.9	1612	2 T30805	duffy protein - mo
45	249.5	4.9	2295	2 C88369	protein unc-52 [im

ALIGNMENTS

RESULT 1

JC7593

SH2 domain-containing phosphatase anchor protein 1a - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C;Accession: JC7593

R;Xu, M.; Zhao, R.; Zhao, Z.J.

Biochem. Biophys. Res. Commun. 280, 768-775, 2001

A;Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.

A;Reference number: JC7593; MUID:21092675; PMID:11162587

A;Accession: JC7593

A;Molecule type: mRNA

A;Residues: 1-255 <XUA>

A;Cross-references: UNIPROT:Q9BZ16; GB:AF319438

C;Genetics:

A;Gene: spapla

A;Map position: 1q21

A;Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3

C;Keywords: glycoprotein

F;27-135/Domain: extracellular #status predicted <EXT>

F;68-115/Domain: immunoglobulin-like #status predicted <IGL>

F;148-169/Domain: transmembrane region #status predicted <TM>

F;195-255/Domain: intracellular #status predicted <INT>

Query Match 10.7%; Score 545.5; DB 2; Length 255;  
Best Local Similarity 54.1%; Pred. No. 4.4e-27;  
Matches 125; Conservative 27; Mismatches 74; Indels 5; Gaps 4;

QY 731 NGLEAQRSEWVT-LKVAVPVSRPVLTLRAPGTHAAVGDLLHCEALRGSPILYRPFHE 789

Db 25 NLRRHKSFLIAPLCLSVFVRPVLTLRSFGQAQAVGDLLHCEALRGSPILYQFYHE 84

QY 790 DVTGLNRSSPS-GGASLNLSTAEHSNGYSCENADNGLGAGQSRSTVLYITGLTANRSGPF 848

Db 85 DVTGLNSSAPSGGAGFNLSTAEHSNGYSCENADNGLGAGQSRSTVLYITGLTANRSGPF 144

QY 849 ATGVAGLLSIAGLAGALLVCWLSRKAGRPASDPSPSDSQEPTVYH-VPAWEE 907

Db 145 TAGVLWGLFGVLGFTGVALLYALFKIGSSATNEPRGASRNPQEFYYSPTDMEE 204

QY 908 LQPVYNNANPRGNVYVSVIRIQEKKHAAVADPRHLRNKSGPIIYSEVK 958

Db 205 LQPVYNNVGSVDVYVSVQVSNQOPE--SSANIRTLLENKDSQVIYSSVK 253

RESULT 2

A41357

Pc gamma (IgG) receptor I (high affinity) form b - human

N;Alternate names: CD64

C;Species: Homo sapiens (man)

C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004

C;Accession: A41357; S03019

Thu May 5 15:11:01 2005

R:Allen, J.M.; Seed, B.  
 Science 243, 378-381, 1989  
 A>Title: Isolation and expression of functional high-affinity Fc receptor complementary  
 A:Reference number: A41357; MUID:89100284; PMID:2911749  
 A:Accession: A41357  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <ALL>  
 A:Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:g31333; PIDN:CRA32536.1; F  
 R:Allen, J.M.; Seed, B.  
 Nucleic Acids Res. 16, 11824, 1988  
 A>Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR)  
 A:Reference number: S03018; MUID:89098339; PMID:2974947  
 A:Accession: S03019  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <ALL>  
 A:Cross-references: EMBL:X14355; NID:g31333; PIDN:CRA32536.1; PID:g31334  
 A:Note: the authors translated the codon ACT for residue 25 as Ala  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein  
 F:117-170/Domain: immunoglobulin homology <IMM>  
 Query Match 8.2%; Score 418.5; DB 2; Length 344;  
 Best Local Similarity 37.0%; Pred. No. 6.2e-19;  
 Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;  
 QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSQKTKWYHR 60  
 DB 7 LLLWV-----PVDGQ-VDTTKAVITLQPPWVSFQETVTLHCEVHLHPGSSSTQWFLN 59  
 QY 61 YLKGKILRETPD---NILEVQESGEYRCQAGSPVHLPDSSASLILQAPLSVF-EG 116  
 DB 60 --GTATQTSPTSYRITSASVNDSEYRCQGLSGRSDPIQLHHRGWLILQVSSRVFTG 117  
 QY 117 DSVVLCRA-KAEVTLNNTIYKNDNVLAFLNKRDTFHIPACIKONGAYRCYTKESCCP 175  
 DB 118 EPLALRCHAWKDKLVNLYRNGKAFKFFHNSNLTKTNISHNGTYHCSGMGKH--R 175  
 QY 176 VSSNTVKIQVQEPFTRPVLRASSFP-ISGNPVTLCETQLSLERSDVLPRFRDDQT 234  
 DB 176 YTSAGISVTVKELFPAPVLNASVTSPLLEGNLVTLSCETKLLQRLQGLQYFSGMSKT 235  
 QY 235 LGLGWSLSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSIQV---QIP 283  
 DB 236 L-RGNTSSEYQILTARREDSGLYWC EAATDGNVLRSPLELEQLVGLQLP 286  
 RESULT 3  
 A39878  
 Fc gamma (IgG) receptor I-A (high affinity) precursor - human  
 N:Alternate names: CD64  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Dec-1991 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: A39878; I70304; B41357; S03018; I57525  
 R:van de Winkel, J.G.J.; Ernest, L.K.; Anderson, C.L.; Chiu, I.M.  
 J. Biol. Chem. 266, 13449-13455, 1991  
 A>Title: Gene organization of the human high affinity receptor for IgG, Fc gammaRI (CD64)  
 A:Reference number: A39878; MUID:91302383; PMID:1830050  
 A:Accession: A39878  
 A:Molecule type: DNA  
 A:Residues: 1-374 <VAN>  
 A:Cross-references: UNIPROT:Q92663; GB:M63830; GB:M63835; NID:g180277; PIDN:AAA35678.1;  
 R:Forges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.  
 J. Clin. Invest. 90, 2102-2109, 1992  
 A>Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.  
 A:Reference number: I55577; MUID:93055454; PMID:1430234  
 A:Accession: I70304  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-374 <RES>  
 A:Cross-references: GB:L03418; NID:g184840; PIDN:AAA36049.1; PID:g292169  
 R:Allen, J.M.; Seed, B.  
 Science 243, 378-381, 1989  
 A>Title: Isolation and expression of functional high-affinity Fc receptor complementary

A:Reference number: A41357; MUID:89100284; PMID:2911749  
 A:Accession: B41357  
 A:Molecule type: mRNA  
 A:Residues: 1-24,'S',26-337,'T',339-374 <AL1>  
 A:Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CRA32537.1; PID:g31332  
 R:Allen, J.M.; Seed, B.  
 Nucleic Acids Res. 16, 11824, 1988  
 A>Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR)  
 A:Reference number: S03018; MUID:89098339; PMID:2974947  
 A:Accession: S03018  
 A:Molecule type: mRNA  
 A:Residues: 1-24,'S',26-337,'T',339-374 <AL2>  
 A:Cross-references: EMBL:X14356; NID:g31331; PIDN:CRA32537.1; PID:g31332  
 R:Perez, C.; Wietzerbin, J.; Benesch, P.D.  
 Mol. Cell. Biol. 13, 2182-2192, 1993  
 A>Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma inte  
 ism.  
 A:Reference number: I57525; MUID:93204964; PMID:8455606  
 A:Accession: I57525  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RE2>  
 A:Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587  
 C:Genetics:  
 A:Gene: GDB:FCGRIA; CD64  
 A:Cross-references: GDB:135911; OMIM:146760  
 A:Map position: lq21-lq21  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane pr  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-292/Domain: extracellular #status predicted <EXT>  
 F:117-170/Domain: immunoglobulin homology <IMM2>  
 F:293-313/Domain: transmembrane #status predicted <TM>  
 F:59,78,152,159,163,195,240/Binding site: carbohydrate  
 Query Match 8.2%; Score 418.5; DB 1; Length 374;  
 Best Local Similarity 37.0%; Pred. No. 6.9e-19;  
 Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;  
 QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSQKTKWYHR 60  
 DB 7 LLLWV-----PVDGQ-VDTTKAVITLQPPWVSFQETVTLHCEVHLHPGSSSTQWFLN 59  
 QY 61 YLKGKILRETPD---NILEVQESGEYRCQAGSPVHLPDSSASLILQAPLSVF-EG 116  
 DB 60 --GTATQTSPTSYRITSASVNDSEYRCQGLSGRSDPIQLHHRGWLILQVSSRVFTG 117  
 QY 117 DSVVLCRA-KAEVTLNNTIYKNDNVLAFLNKRDTFHIPACIKONGAYRCYTKESCCP 175  
 DB 118 EPLALRCHAWKDKLVNLYRNGKAFKFFHNSNLTKTNISHNGTYHCSGMGKH--R 175  
 QY 176 VSSNTVKIQVQEPFTRPVLRASSFP-ISGNPVTLCETQLSLERSDVLPRFRDDQT 234  
 DB 176 YTSAGISVTVKELFPAPVLNASVTSPLLEGNLVTLSCETKLLQRLQGLQYFSGMSKT 235  
 QY 235 LGLGWSLSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSIQV---QIP 283  
 DB 236 L-RGNTSSEYQILTARREDSGLYWC EAATDGNVLRSPLELEQLVGLQLP 286  
 RESULT 4  
 A38096  
 Perlecan precursor - human  
 N:Alternate names: basement  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 12-Jul-2004  
 C:Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736  
 R:Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.  
 J. Biol. Chem. 267, 8544-8557, 1992  
 A>Title: Primary structure of the human heparan sulfate proteoglycan from basement membra  
 tor, laminin, neural cell adhesion molecules, and epidermal growth factor.  
 A:Reference number: A38096; MUID:92235084; PMID:1569102  
 A:Accession: A38096

Query Match	8.1k	Score	412	DB	2	Length	4391
Best Local Similarity	23.2k	Pred. No.	4.8e-17				
Matches	221	Conservative	131	Mismatches	422	Indels	180
Gaps	44						
F;4149-4151/Region: motor neuron attachment (L-R-E) motif							
F;4299-4301/Region: motor neuron attachment (L-R-E) motif							
F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted							
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asa)							
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status pre							
Qy	23	PIIFLOPPWTITVQGERVTLTKCKGPRFYSPOK-TKWVHRYLKGKILLRETPDNL	----	E	76		
Db	2630	PPRISSSTVVEGGTDLNCVVAR--QPAILTYKRGSSLPSSRHQTGSHLRLHQMS	2697				
Qy	77	VOBSGEYRCQAQ-----GSP-----LSSPVHLDFSSASLILQAPLSVF	114				
Db	2688	VADSGEYVCANNIDALEASIVISVPSAGSFSPAGSSMPIRISSSS-----HVA	2739				
Qy	115	EGDSVVLRCRAKEVTLNNTIYKDNVLA--FLNKRTDPHIPHACLKDNQAYRC	--T	167			
Db	2740	EGETDLNCVVPQQAHAQVTHWRKGGSLPSHHQTRGSRRLRLHHVSPADSGEYVCVMGSS	2799				
Qy	168	GKYESCCPV---SSNTVKIQVQPFTRPVL--ASSFQIPISGNPVTLC-----ETQLS	216				
Db	2800	GPLEASVLVTIASGSAVHPAGGAPPIRIEPSSSRVAEGTDLKLCVVPQQAHAQV	2859				
Qy	217	LER--SDVLRFFRRDDOTLGLGWSLSPNQITAMWSKDSGFYWC-----AATMPHSV	-269				
Db	2860	WHRKGNLPAHQVH-----GPIRLNQVSPADSGEYSCQVTCSSGTLEASVL	2907				
Qy	270	ISDSPRSWIOVIPASHPVLTLSPKALNPEGKVTLCHECTQBDLSLRTLYRFYHEG--VP	327				
Db	2908	VTIPESSPGIPAPGLAQPIYIEASSSHVTEGQTLDCVVPQQA--HAQVTVYKRGGS	2966				
Qy	328	LRKSVRCRCASISLSLT--ENSGNYCTADNGLCAKSKAVSLSVTPVSH-----379					
Db	2967	ARHOT----HGSOLRLHLVSPADSGEYVCRAASGPG--PEQEASFTVTPPSEGS	3020				
Qy	380	PVLNLSSPEDLIFEKAVTLHCEAQKGLPILYQFHEDAALERRSANSAGVAISFSL	438				
Db	3021	SPVISIDPSSITVQQQODASFCLIHDAAPISLEWKTRNOELEDNVHISPNCS	3080				
Qy	439	T-AHSGNYYCTADNGFGPQRSKAVSLSTIVPSHPVLTLSSABALTFEQATVTLHCEVQ	497				
Db	3081	TRPSNHGTRCVASNAYGAQS--VNLNVHGPTT--VSVLPEGPVVMVKVKA	3136				
Qy	498	RGSPQILLYQFYHEDMPLMS--SSTPSVGRVSFSLTEGH-----SGNYCYTA	543				
Db	3137	AGBPR-----SSARWTRISSTPA-KLEQRTYGLMDSHAVLQISAKPSDAGTYVCLA	3187				
Qy	544	DNGFGPQGEVMSLFTVPVPSRPIILTRVPAQAVV--GDLLHLHCEAPRGSPPILYW--	599				
Db	3188	QNALGTAQKQVEIVDTGAPCAPOQAEEAELTVEAGHTATLRCATGSPAPTHWSK	3247				
Qy	600	-----FYHEDVTLGSSSAPSGEASFNLSTLTAHSGNYSCEANGLVIAQHS	652				
Db	3248	LRSPLPQWHR-----LEGDTLIIPRVAQDSSQVYCNATS--PAGHAETAILHV	3295				
Qy	653	IVPVSRIILTFRAPRAQAVVGDLLHLHCEALRGSSPILY-WFYHEDVTLGKISAPSGGA	711				
Db	3296	ESP---PYATTVPHEASVQAGETVQLOCLIA-HGTPELTFQW-----SRVGSSLP	3343				
Qy	712	SFNLSL-----TTEHSGIYSCEADNGLEAQSEMTLVAVPVSRIILTRAPGTHA--	763				
Db	3344	TARNELLHFERAAPEDSGRYCRVTNKKVSGAEAFQILLVQGPGLSIPATSI	3403				
Qy	764	-----AVGDILLEHC--EALRGSPILYRFFHEDVTLGNRSSPGGASLNLSTAEH	813				
Db	3404	VTPOLETKSIGASVEFHCAVPSDQGTQL---RWFKEGGQLPPGHSVQDGVLR	3460				
Qy	814	SGNYSCEANGLG-AQRS-ETVTLYITGLTANRSGPFATGAVGGLLSIAGLAAG	865				
Db	3461	QGTYYIQAGHPGWKAQASQALVIALPSVLINRTISVQTVVGHAVEFECLA	3514				

C;Keywords: immunoglobulin receptor  
F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 396; DB 2; Length 336;  
Best Local Similarity 36.1%; Pred. No. 1.5e-17;  
Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

QY 3 LWVI--LLVLAVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60  
Db 10 MWLLTLLWVPVGGVNVNATKAVITLQPPWASIFQKENVILWCESGPHLPQDSSTQWFIN 69  
QY 61 YLQKELRETPD---NILEVQESGEYRCAQGSPLSSPVHLDFFSSAS-LILOAPLSVP-E 115  
Db 70 --GTVVQTSTPSVSIASVAFQDSGEYRCQIGSVSPDPVQLQIHKEDWLLQASRRVLTE 127  
QY 116 GDSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRDTDFHIPACLKNDGAYRCTG---YKE 171  
Db 128 GEPLALRCHGWNKLVYVNVFVRNGSKFRP-SGSGKIALKTNLSHSGIYHCSGMRHRY 186  
QY 172 SCCPVSSNTVKIQVQEPFTRPVLRASSFOPI-SGNPVTLTCTQLSLERSDVLPRFRPFR 230  
Db 187 TSAGVSI-TVKAFPLELFTTPVLRAVSPPFEGSLVTLCETNLLQRPGLQLYFSFV 245  
QY 231 DDQTLGLWSLSPNQITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIP-ASHPV 288  
Db 246 GSKILEYR-NTSSEYHIAEREDAGFYMCVATEDSSVLKHPKLEQLQVLQPOSSAPV 303

RESULT 7  
138346  
elastic titin - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I38346  
R;Label: S.; Kolmerer, B.  
Science 270, 293-296, 1995  
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.  
A;Reference number: A57430; MUID:96026330; PMID:7569978  
A;Accession: I38346  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-7962 <RES>  
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017426  
C;Genetics:  
A;Gene: GDB:TTN  
A;Cross-references: GDB:127867; OMIM:188840  
A;Map position: 2q31-2q31

Query Match 7.7%; Score 396; DB 2; Length 7962;  
Best Local Similarity 24.2%; Pred. No. 1.1e-15;  
Matches 224; Conservative 115; Mismatches 410; Indels 176; Gaps 44;

QY 23 PIIFLOPPWTTVFQGERVLTCTC-----KGRFYSQKTKWYHRYLQKELRE 69  
Db 216 PTFLSRPKSLTTFVGKAAKFTCTVTGTPVETIWKDGAALSPSPNWRISDAENKHILEL 275  
QY 70 TPDNILEVQESGEYRCAQGSPLSSPVHLDFFSSASLIL-----QAPLSVFEQDSV 120  
Db 276 SN---LTIQDRGVYSCKA-----SNKFGADICQELIILDKPHFIKELFVQSAINKKVH 327  
QY 121 LRCRA---KAEVTLNNTIYK---NDNVLAFLNKRDTDFHIPACLKNDGAYRCTGYES 172  
Db 328 LECQVDEDEKVTVTWSKDGKQLPPCKDYKICFEDKIATLEIPKLAKDKSGTYVCTASNEA 387  
QY 173 CCVPSNTVKIQVQEPFTRPVLRASSFOPI-SGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 388 GSSSCSATVTVREPPSFVKKV--DPSYLMPLGESARLHCK-----LKGSPV-IQVTFWFKNN 440  
QY 233 QTLGLWSLSLPNF-----QITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIPAS 285  
Db 441 KEISNTVMTVMFVNSEALIDITDKVVEDSGSYSCNAV---NDVGSDDSCSTEIVIKEPPS 497  
QY 286 HPVLTLSPEKALNFECTKVTILHCT-----QEDSLRT---LYRFYHEGVPLRHK 331

RESULT 5  
A46480  
Fc gamma (IgG) receptor high affinity - mouse  
N;Alternate names: high affinity IgG receptor  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A46480; A43511  
R;Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.  
J. Immunol. 148, 1570-1575, 1992  
A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and  
A;Reference number: A46480; MUID:92166399; PMID:1531670  
A;Accession: A46480  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-404 <OSM>  
A;Cross-references: UNIPROT:P26151  
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC  
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.  
J. Immunol. 144, 371-378, 1990  
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG  
A;Reference number: A43511; MUID:90111035; PMID:2136886  
A;Accession: A43511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-404 <SEA>  
A;Cross-references: GB:M31314; NID:G200752; PIDN:AAA40056.1; PID:G200753  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: immunoglobulin receptor; transmembrane protein  
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 7.9%; Score 402.5; DB 2; Length 404;  
Best Local Similarity 36.3%; Pred. No. 7.7e-18;  
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY 3 LWVI--LLVLAVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60  
Db 10 MWLLTLLWVPVGGVNVNATKAVITLQPPWASIFQKENVILWCESGPHLPQDSSTQWFIN 69  
QY 61 YLQKELRETPDNL---EVOESGEYRCAQGSPLSSPVHLDFFSSASLILQAPLSVP-E 116  
Db 70 --GTVVQTSTPSVSIASVAFQDSGEYRCQIGSVSPDPVQLQIHKEDWLLQASRRVLTEG 127  
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRDTDFHIPACLKNDGAYRCTGYESCCP 175  
Db 128 EPLALRCHGWNKLVYVNVFVRNGSKFQF-SSDSEVAILKTNLSHSGIYHCSGTGRH--R 184  
QY 176 VSSNTVKIQVQEPFTRPVLRASSFOPI-SGNPVTLTCTQLSLERSDVLPRFRFRDDQ 234  
Db 185 YTSAGVSI-TVKAFPLELFTTPVLRAVSPPFEGSLVTLCETNLLQRPGLQLYHFSFYVGSKI 244  
QY 235 LGLWSLSPNQITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIP-ASHPV 288  
Db 245 LEYR-NTSSEYHIAEREDAGFYMCVATEDSSVLKSPLEQLQVLQPOSSAPV 298

RESULT 6  
I48471  
Fc gamma (IgG) receptor high affinity - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I48471  
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gath  
Science 260, 695-698, 1993  
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig  
A;Reference number: I48471; MUID:93242399; PMID:8480181  
A;Accession: I48471  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-336 <RES>  
A;Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology

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Db 498 F-IKTLBPADIV--RGTNALLQCVSGTGPFEISWFKDKQIRSKYRLFQ-----K 548
Qy 332 SVRCERGASISFSLTITNSGNYCTADNGLCAKPSKAVSLVTPVGHVPLNLSSPDLI 391
Db 549 SLVCLC-----IFSNSADVGVEYCVANVEVKCCGMATHL-----LKEPPTFKVVDLI 599
Qy 392 FEGAKVTLHCBAQGSILPIL-----YQFHEDAALERRSANSAGGVAISF--SLTAHS 443
Db 600 ALGGQVTLQAAVRSSEPISTVMKQGEVIREDKIKMSFSN---GVAVLIIIPDVQISFG 656
Qy 444 GNYCTADNCGPQPSKAVSLISITVPVSHPVLTLSAEAL--TPGATVTLHCEVQSRPQ 502
Db 657 GKYTCLAENAGSQTSGELI-----VKPEAKIIERAELIQVTAGDPATLEYTV--AGTPE 710
Qy 503 ILYQFYHEDPMLWSSTPSPVGRVSF-----SFLTEGH--SGNYCYCTADNGFGPQSRSEV 554
Db 711 LKPKWYKDRPLVASKK---YRISFKNNVAQLKFYSAEHLHDSGQYTFEISNEVGSSCET 767
Qy 555 VSLFVTVVPSRPILTLVPRQAQVVGDLLELHCEAPRGSPPIVWFYHEDVTLGSSAPS 614
Db 768 TFTVLDRDIA--PFPTKPLRNVDVSVNGTCRLDCKIAGSLPMRVSWF--KD---GKEIAAS 821
Qy 615 G-----GEASFN--LSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPILTFR 665
Db 822 DRVRIAFVEGTASLEIIRVDMNDAGNFTCRATNSVSGKDS-----SGALIVQEPSPFTK 876
Qy 666 PRAQAVVGDLLELHCEALRGSSPI--LYWFYHEDVTLGKISAPSGGG-----ASFNL 715
Db 877 PGSKDVLPGSNAVCLKSTFQSTPTIRWF-----KGNKELVSGGCVYTKAELESLEL 930
Qy 716 SLT--TEHSGIYSCADN---GLEAQRSEMTLKVAVPSRPVLTFRAPGTHAAVGDLLLEL 771
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Qy 772 HCEALRGSPILYFPHEDVTLGNRSS-----PSGGASLNLIS--LTAHSGNYSCEADNGL 825
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Db 1044 GSDHCSSIVV-----KESPYFT 1061

RESULT 8
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heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 265, 22939-22947, 1991.
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
R;Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogel, G.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
R;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
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A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
R;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.

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Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,X',1276,X',1278-1279 <SCH>
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F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
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F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
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Best Local Similarity 23.0%; Pred. No. 6.1e-14;
Matches 215; Conservative 108; Mismatches 413; Indels 199; Gaps 45;
Qy 23 PIIFLOPPTVTVQGERVTLTKGFRFYSPOKT-----KWHRYLKGKEILRETQDNI 74
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Qy 75 LEVQESGEVRCQAQ-----SPLS-SPVHLDFSSALLOAPLS 112
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Qy 113 VFEQSDSVLRCAKAEVTLNNTIYKNDNVLAFLNKR--TDFHIPHACLKQNGYRC--- 166
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Qy 167 -TGKSCCPSVNTVKIQVQEPFTRPVL--ASSQPIISGNPVTLTC-----ETQLSL 217
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Qy 267 HSVI-----SDSPRSMIQQVIPA---SHPVLTLSPEKALNFEQTKVTLHCETQ--EDSLR 316
Db 2226 ASVLVTEIASPSF-----IPAGLAQPVYIESSSHLT--EGQTVDLKCVVPGQAHQ 2277
Qy 317 TLRYFYHGVPLRHKVRCERGASIS--FSLTTNSGNYCTADNGLGAKPSKAVLSVTV 375
Db 2278 VTHKRGSSLPARHQT---HGSLLRLYLQSLPADSGEYVCQVAG--SSHPHEASFKLTV 2331
Qy 376 PVSH-----PVLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAALEERSAN 427
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Qy 428 SAGGVAISF---SLTAHSGNYYCTADNCGFGPQPSKAVSLISITVPVSHPVLTLSAEAL 483
Db 2392 SPNGSIITIVAPGPATMEPTA---CVASNVYGAQS--VNLNVHGPTT--VSVLPEGPVH 2445
Qy 484 TFEQATVTLHCEVQSRQPILYQFYHEDMPLWSSSTPSPVGRVSFSLTEGH----- 535
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Qy 536 ----SGNYCYCTADNGFGPQSRSEVVSIFV---TPVSRPILTLVPRQAQVVGDLLELHCE 588
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Qy 589 APRGSPPIVWFYHEDVTLGSSAP-----SGEASFNLSTAHSNGYSCEANGLVA 642
Db 2556 ATGNPPTTHW-----SKLRAPLDPWQHRIENGLVTPRVAAQDQSGQVINCATNS--A 2605
Qy 643 QHSD--TISLSVIVPSRPILTFRAPRAQVVGDLLELHCEALRGSSPILY-WFYHEDVTL 700

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F/340-388/Domain: immunoglobulin homology <IMW1>  
F/424-478/Domain: immunoglobulin homology <IMW2>  
F/602-620/Domain: transmembrane #status predicted <TRA>  
F/621-738/Domain: intracellular #status predicted <CYT>  
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Best Local Similarity	22.6%;	Pred. No. 2.7e-14;		
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Qy	298	N	-----FEGTKVTHCETOEDSLR	TLRYFRYHGBVPLRHKS	VRCERGASISFSLTTE	348
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	54	TLQCFADVSTTSHVKPOHQL	-----FYKDDVLF	-----YNISSMKSTESYFIPE	98	
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	349	-----NSGNYCYCTADNG	IGLAKPXS	KAVSIVTVPVSHPVNL	SSPEDLIFEGAKVTLHCEAQ	404
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	99	VRIYDSGTGYKCTVI	NNKKTETAYQ	LLVE-GVPSPRVTL	DKKBAI--QGGIVRWNC	SVP 155
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	405	RGSLPILYQFH	-----HEDAALERSANS	AGGVAISFL	TAHSG-----NYVCTAD--NGGF	455
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	156	EKAAPHIPTIEKLE	NEKNMKVLKREKNS	RQDNFVILEFPVEEQ	DRVLSFRQARII	SGIH 215
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	456	PORS	-----KAVSLSITVPSH	PVLTLSAAELTFEGAT	VTLHCEVQ-----RGS	POLLYQF 507
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	216	MOTSESTKSELVTVTES	SPKPHISPT-GMIMEGA	QOLHIKCTIQVTHLAQ	EFPEI	IIQ- 273
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	508	YHEDPMLWSSTPS	GVRSFSLTEGHSGNY	CYCTADNGFGPQRSE	VVLSFVTPV--VSR	565
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	274	--KDKAIVAHNRHGN	KAVYSVMWVE-HSGNYT	CKVESS---RISKVSSI	VVNITELFSK	327
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	566	PILTLRVPRAQAV	VGDLLELHCEAPRGS	PPILYFWFYHEDVT	LTGSSAPSGGEAS	FNLSLT 625
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	328	PELESSFTHLDO--GER	NLSCSIP-GAPPAN	FTIQKEDTIVSQTQ	-----DET	KIAS 377
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	626	AEHSGNYSCEAN	GLVIAQHSDTISLS	VIVPVSRPILTF	PRAQAVVGDLLELHCEAL	URG 685
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	378	KDSGTIYCTAGIDK	VKKVKSNTVOIVC	EMLSQPRISYDA-QFEV	IKQOTIEVR	CESIG 436
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	686	SSPILYWFYHEDVT	LKGISAPSGGAS	FNLSLTTEHSGIY	SCEDN--GLEAQRSE	MTL 743
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Db	437	TLPISYQLLTKTS	SKVLENTKNSND	PAVFKDAPTE	DVE--YQCVADNCH	SHAKMLSEVLV 494
		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
Qy	744	KVAVPVSRPVLTL	RAPGTHAAVGDLLELHCEAL	RGSPLILYRFFHEDVT	LTGNRRSP	SGGA 803
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Qy	804	SINLS	-----LTAHSGNYSC	-----EANGLQAQRSE	VITLYITGLTANRSP	FPATG 851
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		WGLVLT	-----WGLVLT	-----WGLVLT	-----WGLVLT	
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RESULT 10  
JH0371  
B-cell adhesion protein CD22 beta splice form precursor - human  
N;Alternate names: B-cell membrane protein CD22  
C;Species: Homo sapiens (man)

## RESULT 10

RESUL  
JH0371

U0371 B-cell adhesion protein CD22 beta splice form precursor - human

N:Alternate names: B-cell membrane protein CD22

N; Alternate names: B-cell men  
C: Species: Homo sapiens (man)

Db	2606	GHTAEPVVLHVESP---PYATIIPHTSAQPNLVQLQCLA-HGTPPLITYQW-----SLV	2656
Qy	701	GKISAPSGGGAGFNLSL---TTEHSGIYSCEADN---GLEA-----ORSEMVTILKVAVP	748
Db	2657	GGVLPEKAVVRNQLLLETFVEDSGRYRCQVSNRVGSAEFAQVLVQSSSNLPTDTSIP	2716
Qy	749	-VSRPVLTLRAPGTHAAVGDLLELHCEA--LRGSPILLYRPFHEDVTILGNRSSPSGGASL	805
Db	2717	GGSTPTVQVTPQLETNIGASVEFFHCAPVNERGTHL---RWLKEGGQLPPGHSHVQDGVLR	2773
Qy	806	NLSLTAHSGNYSCEADNGLGQAQRSTVTLYITGL	840
Db	2774	IOMIDONCOGYVVCOR-HGPMWCGAQAQTAQILVQAL	2807

## RESULT 9

A40096  
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N;Alternate names: intercellular adhesion protein, carcinoembryonic antigen; leukocyte  
C;Species: Homo sapiens (man)  
C;Date: 16-Oct-1992 #sequence\_revision 16-Oct-1992 #text\_change 09-Jul-2004  
C;Accession: A40096; A48720; JI0142; A43536; A40549  
R;Newman, P.J.; Berndt, M.C.; Gorski, J.; White II, G.C.; Lyman, S.; Paddock, C.; Muller  
Science 247, 1219-1222, 1990  
A;Title: PECAM-1 (CD31) cloning and relation to adhesion molecules of the immunoglobulin  
A;Reference number: A40096; MUID:90193682; PMID:1590453  
A;Accession: A40096  
A;Status: nucleic acid sequence not shown  
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A;Cross-references: UNIPROT:P16284; GB:M28526; NID:G189775; PIDN:AAA36429.1; PID:G189776  
A;Note: the nucleic acid sequence is shown in reference A40549  
R;Tang, D.G.; Chen, Y.Q.; Newman, P.J.; Shi, L.; Gao, X.; Diglio, C.A.; Honn, K.V.  
J. Biol. Chem. 268, 22883-22894, 1993  
A;Title: Identification of PECAM-1 in solid tumor cells and its potential involvement in  
A;Reference number: A48720; MUID:94043056; PMID:8226797  
A;Accession: A48720  
A;Molecule type: mRNA  
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A;Cross-references: GB:S66450; NID:G435945; PIDN:AAB28645.1; PID:G435846  
A;Experimental source: colon adenocarcinoma  
A;Note: sequence extracted from NCBI backbone (NCBIN:138975, NCBIP:138976)  
R;Simmons, D.L.; Walker, C.; Power, C.; Pigott, R.  
J. Exp. Med. 171, 2147-2152, 1990  
A;Title: Molecular cloning of CD31, a putative intercellular adhesion molecule closely  
A;Reference number: JI0142; MUID:90278365; PMID:2351935  
A;Accession: JI0142  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
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A;Note: the extracellular domain contains four contiguous C2-like immunoglobulin domains  
R;Stockinger, H.; Gado, S.J.; Eher, R.; Majdic, O.; Schreiber, W.; Kasinrer, W.; Straus  
J. Immunol. 145, 3889-3897, 1990  
A;Title: Molecular characterization and functional analysis of the leukocyte surface protein  
A;Reference number: A43536; MUID:91060975; PMID:1700999  
A;Accession: A43536  
A;Molecule type: mRNA  
A;Residues: 1-124, 'V', 126-562, 'N', 564-669, 'G', 671-738 <STO>  
A;Cross-references: GB:M37780; NID:G187239; PIDN:AAA36186.1; PID:G187240  
R;Albelda, S.M.; Muller, W.A.; Buck, C.A.; Newman, P.J.  
J. Cell Biol. 114, 1059-1068, 1991  
A;Title: Molecular and cellular properties of PECAM-1 (endoCAM/CD31): a novel vascular  
A;Reference number: A40549; MUID:913340830; PMID:1874786  
A;Contents: annotation  
A;Comment: This protein is a widely distributed glycoprotein on endothelial cells, plate  
C;Genetics:  
A;Gene: GDB:PECAM1  
A;Cross-references: GDB:696372  
A;Map position: 17q23-17q23  
C;Keywords: cell adhesion; glycoprotein; phosphoprotein; transmembrane protein  
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442 CNYNSSNPSVT---RYEWKPHGAWEEBSGLVKIQNVGWDNTTIACARCNSWCS----- 492
549 PORSEVVLSPTVPVPSRPILTLRV-PRAQAVGDLLELHCEAPRGSPPILYWPFYHEDVTL 607
493 --WASPVALNVQY-APRDVVRVKIKPLSEIHSNGSNVSLQDCFSSHPKEVQVFFWKNRGL 544
608 GSSAPSGGGEASPNL-SLTAHSGSNVSCYEANGLVAQHSDTISLSTVTPVPSRPILTLFRAP 666
550 -----LGKESQLNPSIISPEDAGSYSCVWNNSIGQTASKAWTLEVLV-APRRLRVMSWP 602
667 RAQAVVGDLLELHCEALRGSSPILY-WFYHEDVTLGKISAPGGGGASFNLS-LTTEHSG 723
603 GDQVMEKGSATLTACES-DANPPVSHVYTWFDWNQSLPHHS-----QKRLPEPVKVQHS 655
724 IYSCDADNGLEAORSEWMTLKVAVPVSRPVLTLRAPGTHAAVGDLLELHCEALRGSPIL 783
656 AYWCQGTNSVGRKSRPLSTLV-----677
784 YRFHEDVTLGNRSSPSGGASNLSTABHSGNVSCDADNGLAQRSETVTLVITGLTAN 843
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725 SSGQ-SFFVRNKVKRRAPLSEGHPSLGCYNPMMEDGISYTTLAFPENNIPTGTDAESSEM 783
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T20992  
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C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T20992; T24733  
R:Sulston, J.  
submitted to the EMBL Data Library, December 1994  
A/Reference number: Z19355  
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A/Status: preliminary; translated from GB/EMBL/DBJ  
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A/Experimental source: clone F15G9  
R:Kershaw, J.  
submitted to the EMBL Data Library, December 1994  
A/Reference number: Z19929  
A/Accession: T24733  
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A/Experimental source: clone T09B9  
C/Genetics:  
A/Gene: CESP:F15G9.4a  
A/Mat position: X  
A/Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;  
2512/2; 2593/3; 2699/3; 2759/1; 2852/3; 2889/3; 2913/3; 2941/1; 2967/3; 2991/  
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Db 430 PRAFMSPHGE-FVGRDLNLSC-----TVESASATYIVWKTGDIIGLGFVHNHTDS 482





QY 563 ---VSRPILTLRVPRAQAVV-----GDLELHCEAPRGSPPILYWYFHHEDVTLGSS 610  
DB EGGIVFKPTISGMDKHAIVAVNSTHVDLGEFAIPCWVGSTPPPIITWLD-----GRP 1040  
QY 611 SAPSGGEASFNLSLTAE-----HSGNYSCEANGLVAQHSDTISLSVIPVSRP 659  
DB 1041 ITN-----SRDFTVADNTLIVRKADKSYGVVTCQATNSA-----GDNEQKTIIRINWTP 1092  
QY 660 ILTRAPRAQAVVGDLELHCEALRGSSPILYWF-----YHEDVTLGKISAPSGG 709  
DB 1093 MISPGQSSFNWVDDLTFTPCDVVGDPKVITLLDDKPPTEGVWNE-----GSLTIP--- 1146  
QY 710 GASFNLSLTTEHSGIYSCDADNGLEAQRSEWILKVAVPVSRPVLTRAPGTHAAVGDLL 769  
DB 1147 -----NVNBAHRGTFTCHAQNA-AGNDTRVTLTVH-----TTPTTNAENOEKIALQNDI 1196  
QY 770 ELHCEA-LRGSPLILYRFFE-----DVTIGNRSSPGGASLNLSLTAEHSGNYSCEADNGLG 826  
DB 1197 VLSCPAPALPPVRLWYIEGKIDSLIPHITREDGALVLQNVKLENTGVFVCOVSN-LA 1255  
QY 827 AORSETVTLXI 837  
DB 1256 GEDSLSVTLTV 1266

RESULT 13  
I49583  
differentiation antigen - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49583  
R:Law, C.  
J. Immunol. 151, 175-187, 1993  
A:Title: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterization  
A:Reference number: I49583; MUID:93315834; PMID:8100843  
A:Accession: I49583  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-862 <RES>  
A:Cross-references: UNIPROT:P35329; GB:L16928; NID:G348965; PIDN:AAA02562.1; PID:G348966  
C:Genetics:  
A:Gene: CD22

Query Match 6.5%; Score 330; DB 2; Length 862;  
Best Local Similarity 19.9%; Pred. No. 7.5e-13;  
Matches 212; Conservative 137; Mismatches 348; Indels 366; Gaps 46;

QY 3 LWILLVLAPVSGQA-----RTRP-----IIFLPQ 29  
DB 6 LWLLILGHAAQAQYSSANDWTVDHPQTLPAWEGACIRIPCKYKTLPLKARLDNILLFQN 65  
QY 30 PWTTVFQGERVTLTCKGFRFYSQKTKWH-----RYLGKEILRETPDNI-----LEV 77  
DB 66 -----YEFDKATKKFKGTGLYLNKAEPYLPKORRVTLGNSI-----DNCTLIKHPIRA 115  
QY 78 QESGE---YRCAQAGSPPLSPVHLDFSSASL---ILQAPLSVFEGSDSVVLRCAKAEVTLN 133  
DB 116 NDSGNLGLRTAGTERMEIHLNVSEKPPQYIQMPEIRESQSVTLTC-----GLNF 169  
QY 134 TIYNDNLVLAFLNKRTDFHIFACLKONGAYRCITGYKESCCPVSSNWTVKIQVEPTRPV 193  
DB 170 SCEPYDILLQWF-----LEDS---KITSVTPSVTSITS-SVTSSIKNVVTEK 213  
QY 194 LRASSFQP-LSGNPVTLTCTQLSLERSDVLFRFRDDQTLGLGWSLSPNFQITAMWS 252  
DB 214 L-----TFQPKWTDHGKSVKQCVQHSSE-----VLSERTVRLDVVKPKLEI----- 255  
QY 253 KDSGFYCKAAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFEKGKVTLLHCETOE 312  
DB 256 -----KVNPTVEKXNSVTMTCRVNSN 278  
QY 313 DSIURLT-YRPHYHGVPLRHKSVCERGAS---ISFSLTENSNNYCTADNGLGAKPSKAV 369

DB 279 PKLRTVANWFKDGRPLEDOLEBQOQMSKLIHLSVTKMRGKYRCQASNDIGPGESEV 338  
QY 370 SLSV-TVPVSHPVNLNLSPPEDLIFEAGAKVTLHCEAQRGSLPILYQFHEDHAALERRSANS 428  
DB 339 ELTVHYAPBSRVHIYSPAE---EGSVELICESLASPSATNTYTWYHNRKPIPGDTQEK 395  
QY 429 AGGVALISFSLTAHSGNYICTADNGFG-----PORSKAVLSLTIVPVSHP 473  
DB 396 LRIPKVS---PWHAGNYSCLAENRLGHGKIDQEAKLVDHYAPKAVTTVIQSET-----P 446  
QY 474 VLTLSAAELTREGATVTLHCEVQGRSPQILYQFYHEDMPLWSSSTPSVG-----RVSPS 528  
DB 447 IL-----EGDSVTLVCRYNSSNPDTVSRWN---PQSGSVLKPGLVRIKQIKTWD 493  
QY 529 FSLTEHSGNYYCTADNGFGPQRSEVVSJFVTVPVS-RPILTLRV-PRAAVAVGDLLLELH 586  
DB 494 SMPVSCAACNHC-----SWALPVILNVHYAPROVKVLKVPASEIRAGORVLLQ 543  
QY 587 CEAPRGSPPILYWYFHHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCEANGLVAQHSD 646  
DB 544 CDPAESNPAAEVRPFWKKN---GSLVQEGRYLSFG-SVSPEDSGNYSNVMNNSIGETLSQ 598  
QY 647 TISLSVIVPVSRLPILTRAPRAQAVVGDLELHCEALRGSSPILYWYFHHEDVTLGKISAP 706  
DB 599 AMNLQVLY-----APR----- 609  
QY 707 SGGGASFNLSLTTEHSGIYSCDADNGLEAQRSEWILKVAVPVSRPVLTRAPGTHAAVG 766  
DB 610 -----RLRYSI-----SFGDHVMEG 624  
QY 767 DLELHCEALRGSPPILYRFFHHEDVTLGNRSSPGGASLNLS-LTAEHSGNYSCEADNGL 825  
DB 625 KKATLSCESDANPPISQYTWFS---SGQDLHSSGQKLRLPLEVQHTGYSYRCKGTNGI 680  
QY 826 QAORS---ETVTLTYITGLTNRSPFFATGVAGLLSIAGLAA-CALLLYCW----- 872  
DB 681 GTGESPPSLTVIYSPETIGKR--VALGL-GFCLTICILAIWGMKIQKKWKQNRSQOGLQ 737  
QY 873 -----LSRKAGRKPSADPARS-----PDSDS-----QBPTYHN-----VPA 904  
DB 738 ENSSGQSFFVRNKKARTPLSEGOQGCYNPAMDVTVSVALIRFPFSDMHNAGDAGTTPA 797  
QY 905 WEELQP-----VYTNN-----PRGNVNVYSEV 927  
DB 798 TOAPPNNNSDVSITYSVIQRPMGDYENVPNSCPDESEIHYSEL 840

RESULT 14  
T09402  
immunoglobulin-like protein IGSF1 - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09402  
R:Mazzarella, R.; Pengu, G.; Jones, J.; Jones, C.; Schlessinger, D.  
Genomics 48, 157-162, 1998  
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.  
A:Reference number: Z16665; MUID:98190514; PMID:9521868  
A:Accession: T09402  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1327 <MAZ>  
A:Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:G2645889; PIDN:AACS2057.1; PID:G2645889  
C:Genetics:  
A:Gene: iggf1  
A:Map position: Xq25

Query Match 6.5%; Score 330; DB 2; Length 1327;  
Best Local Similarity 21.8%; Pred. No. 1.3e-12;  
Matches 256; Conservative 159; Mismatches 401; Indels 358; Gaps 61;

QY 13 VSGQPARTPRPIIFLOPPWTTVFOGERVTLTKG-----FRFYSQKTKWYHYLG 63  
DB 212 VAGLY---PKPTLTAH-PGPIMAPGSLNRCQGPITYGMTFALMRVEDLEKS-FYHK--- 263

875 RKAGR-----KPSDPAKSPSDSDSQ 895  
1286 ETDGRDQTALBECNOGEGPT-PANSPSSTSQR 1318  
RESULT 15  
S50065  
sialoadhesin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: S50065  
R;Cocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc  
EMBO J. 13, 4490-4503, 1994  
A;Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells v  
A;Reference number: S50065; MUID:95009950; PMID:7925291  
A;Accession: S50065  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1694 <CRO>  
A;Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:g557253; PIDN:CAA85290.1; PID:g55722  
Query Match 6.4%; Score 327; DB 2: Length 1694;  
Best Local Similarity 20.1%; Pred. No. 2.9e-12; Indels 410; Gaps 48;  
Matches 236; Conservative 125; Mismatches 401;  
18 ARTPRPIIPFPWWT-----TVQGERVTLTCKFRFFYSPOKTKWYHR---Y 61  
224 AHSRKEVYLVQPHAPKGVILLSSGRNLPDGPVTLTCRVNSSYPVAVSQWARGDVN 283  
62 LGKEILRETNDILEV-----QSGGEYRQCA---QGSPLSPVHLDPSSASLILQAPLSV 113  
284 LG-----VTGHVLRLFSAAMNDGAYTQATNDMGSLSVPSLSLHVFAEVKNNPAGPV 337  
114 PEGDSVVLRCRAKAEV--TLNNTIYKNDNVLAFLNKTDFHIFACLKONGAYRC----- 166  
338 LENETVLLCTPKAPQELRYKSWYKHHLEDAHAAT-LHLPAVTRADTGFYFCEVQNA 396  
167 -----TGKES-----CCPVSS----- 178  
397 QGSRSSPLSVVVRYPPLTPDITTFLETOAGLVGLHCVVSEPLATVLSHGGLTASN 456  
179 -----NTVKIQVOE-----PFTFVPLRA-- 196  
457 SGENDFNPRFISSAPNSLRLEIRDLQPADSGEYTCVAVNSLGNSTSSLDPYANVARLLI 516  
197 --SSFOPIISGNPVTLTCTQLSLERSDVP-LRFRFRDDQTGLGWSLSPNFOITAMSKD 254  
517 NPSAEVVEGQAVTLSCRSGL---SPADTRFSWYLVNGLALLEGSSSS--LLLPAASSTD 570  
255 SGFTYCKAATPHSVISDSPRSQWQVQIPASHVLT--LSPEKALNPGTKVTTLHCETQE 312  
571 AGSYTCRTQAGNTSGPSLP-TVLTVFYPKPKPTTARLDLDTSGVGGRGILLCHVDS 629  
313 D---SLRTLRYRHEGVPLRHKSVCRCGASISFSLTT-----ENSGNYICTADN 359  
630 DPPAQLRLHKHGVATSLPSCGSCSQRKTVSRNSLHVIEIQFVLEDEGVLCESAN 689  
360 GLGAKPSKAVSLSVTVFVSHVNLNSSLPEDLIFEGAKVTLHCEAQ----- 404  
690 TLG-NSSAAAFNAKATVL-----VITFNTLREGTEANLTCNGNOEVAVSPANFSWRN 743  
405 -----RGSPLI--LYQFHEDAA-----LERRSANSAGGVAISFSLTAE----- 441  
744 GVLMTOGSLETVRLQLLARTDAVYACRLLTEDGQLSAPVLSVLYAPDPKLSALLDV 803  
442 ---HSGNYICTADN-----GFGPQR-----SKAVSLSVTVVSHV 474  
804 GQGHMAVFICTVDSYPLAHLSPRGDHLIATNLEPQPSHGRIOAKATANSIOLEVREG 863  
475 LT-----LSSAEALTF-----EGATVTLHCVQRG-SPQILY 505  
864 LVDSGNVHCATNILGSANSLFFQVRGAWRFTITELREGQAVVLSCCVPTGVSSEGTYS 923

64 KEILRETPDNI-----LEVOESGEYRC-----QAQGSPLSSPVHL-----DFSSASLILQAPL 111  
264 KTIKNEA--NFFQSKIKQDTGHVLCFYDYASRGSLSDVLKIWTDTTPKTKWLLARPS 321  
112 SYFE-GDSVVLRCRAKAEVTLNNTIYK--NDNVLAFL-----NKRTPDFHIPHACLKONGA 163  
322 AVVQMGQVSLRCRGPDV-GVGLALYKKGEDKPLQFLDATSIDNTSPFLNNVTVSYDTGI 380  
164 YRC---TGKESCCPVSNVTKIQVQBEPFVPLRA---SSFOPIISGNPVTLTCTQLSL 217  
381 YSCHYLLTKWTSIRPESHNTVLMVVDKPKFSLSAWPSVFK--LGKAITLQCRV----- 434  
218 ERSDVPLRFRFRDQDTGLGWSLSPNFOITAMWSKDSGYWCKAATPHS----- 268  
435 --SHPVLEFSLEWEERETQKFSVNGDFIISNVGDKGTGYSYCSRVVETHPINWHRSEP 492  
269 -----VISDSPR-----SWI----- 278  
493 LKLMGPAGYLTWNYLVNLAIRLSLMQLVALLVLMIRWKCRRLRIRAEAWLLGTAQGV 552  
279 -----OVQIPASHPVL-----TLSPEKALNPEGTKVTLHCET 310  
553 MLFIVTALLCCGLCNGVLIEETEIVMTPKPELMAETNPPLAPWKNL-----TLWCRS 605  
311 QEDSLATLRYFYHEG--VPLRHKSVCRCGASISFSLTTENSNGNYICTADNGLG-AKPS 366  
606 PSGSTKE-FVLLKDGKGWATRAPSOV-RAAPFLGALTQSTGTSYHCHSWEEMAVSEPS 663  
367 KAVSLSVTVVSHVPLNL-----SSPEDLIFE-----G 394  
664 EALELVGTDILPKFVISASTIRGQELQRLCKGWLAGMGFALYKEGEQEPVOOLGAVGRE 723  
385 -----SSPEDLIFE-----G 394  
724 AFTTIQMEDKDGNVSCRTHTEKRPFKWSEPELELVIKEMYPKPFKTWASPVVTPG 783  
395 AKVTLHCEAQRGSLP-ILYQFHEDAAALERRSANSAGGVA--ISFSLTAEHSGNYICT-A 450  
784 ARVTFNCSTPHQMSFILYKDGSEIASDRSWASPGASAAHFLIISVIGDGGNYSERY 843  
451 DNGFGPORSKAVSLSVTVVSHVPLTSSAEATFEAGATVTLHCEVQRGSPQ-----ILY 505  
844 DFSIWSEPSDVELVWTFEPKPTL-LAQPGVVPFCKSVILRCQ---GTFQGRFALLQ 899  
506 QFYHEDMPLWSSSTPSVGRVSFSESL-TEG--HSGNYIC---TANGFGPQSEVVSFLF 558  
900 EGAAH--VPL---QFRSVSGNSADFLHTVGAEDSGNYSYCYVYETTMNSRGSYLSMPLMIW 954  
559 VTVVPSRPILTLRVPRAQAVVGDLELHCEAP-RGSPILYWFYHED-----VTLGSSSA 612  
955 VTDTPPKPWL-FAPFPSSVPMQNVTLWCGRFVHGVGVIIL-----HKEGEATSMQLWGSTS 1009  
613 PSGGEASFNLSLTAHSGNYSYSC---EANNGLVAQHSDTISLSVIVPSRPILTFRAPRA 668  
1010 NDGAFFITNIGTS--MGRIYSCCHVDPWTSSIKIQPSNTLELLVTLGLLPKPSL-LAQPGP 1066  
669 QAVVGDLELHCEALRGSSPILYWFYHEDVTLGKI-----SAPSGGASFNLSL 717  
1067 MVAPGENMTLQCC--GSLP-----DSTFVLLKEGAQEPLEQRPSPGYRADFWMPAV 1115  
718 TTEHSGIYSC--EADNGLEAQRSEMVTLKVAVPVSRPRLTLRA-PGTHAAVGDILLELHCE 774  
1116 RGEDSGIYSCVYLDSTPFAASNHSDSLIWIWTDKPKPSLSANFSTFWLKGDKITLQCC- 1174  
775 ALRGS-PLILYRFFHEDVTLGNRSSPGGASINLSLTAHSGNYSYSC-----EADNGLGAOR 829  
1175 --RGPLPGVEFVLEHDEGEAPQFSEGDGFVIN-NVEKGIGNYSYCSYRLQAYPDINSEP 1231  
830 SETVLYITGLTANRSGPATG-----VAGLLSIAGLAAGALLCYWL-----S 874  
1232 SDPLEL-----VGAAGPVAQCEQTVGNIVRSSLIIVVVVALGVLAIEWKWPRLRTRGS 1285

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Qy 506 QFYHEDMPLNSSSTPSVGRVUSFSLTEHSGNYCTADNGFGPQRSEVUSLFTVTPVSR 565
Db 924 SWYQDGRPL-QESTSSTLRIA-AISLRQ--AGAYHCOA-----QAPDTAIASLAAPVSL 973
Qy 566 PI-LTLRPRAQAVVGD---LLELHCEAPRGSPILYWFYHED---VTLGSSSAPSGG 616
Db 974 HVSYTPRHVTLSALLSTDPERLGHLCVSV-QSDPPAQLQLFHRNRLVASTLQGADELAGE 1032
Qy 617 EASFNLSL-----TAHSGNYSCEANN--GLVAQHSDTISLSLVIVPVSRPILT 662
Db 1033 NPLRHVTVLNPLNELRLQIHFFPELEDGGTYTCEASNTLQASAAADFDAQAVRTV----- 1086
Qy 663 FRAPRAQAVVGDLELHCEALRGSSPILYWFYHED----- 697
Db 1087 --WPNATVQEGQQVNLTC-----LVWSTHODSLSYTWYKGQQLGARSITLPSVK 1135
Qy 698 -----VTLGKISAPSGGGASFNL----- 715
Db 1136 VLDATSVRCGVGLPGHAPHLSRPVTLDVLHAPNRLRITYLLETQGRQALVLCVDSRPP 1195
Qy 716 -SLTTEH-----SGIYSCADNGLAQORSEMTLKVA 746
Db 1196 AQLTSLHGDQLVASSTEASVPNTLRLLELQDPRSPNEGLYSCSAHSPGKANTSLELLEGG 1255
Qy 747 VPVSRPVLTLRAPGTHAAVGDLELHCEALRGSPILYRPFHEDVTLGNRSSPSGGASLN 806
Db 1256 VRVK-----MNPSSGVPEGEPTVTCEDPAALSSALYANFHN---GHWLQEGPASSLQ 1305
Qy 807 -LSLTAHSGNYSCEADNGLAQORSEMTVLYI 837
Db 1306 FLVTRAHAGAYFCQVHDTQGRSSRPASIQI 1337
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Search completed: May 4, 2005, 11:39:23  
Job time : 35.6362 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 131.777 Seconds  
(without alignments)  
3796.562 Million cell updates/sec

Title: US-09-724-254A-41  
Perfect score: 5116  
Sequence: 1 MLLWVILLVLPVSGGFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	5115	100.0	977	2	Q96RD9
2	2091	40.9	437	2	Q8NF56
3	1563	30.6	734	2	Q96LA4
4	1559	30.5	734	2	Q96P31
5	1559	30.5	742	2	Q8N6S2
6	1549	30.3	740	2	Q96P29
7	1205.5	23.6	639	2	Q96P30
8	1067	20.9	582	2	Q80WN2
9	1067	20.9	595	2	Q68SN8
10	931.5	18.2	508	2	Q96LA5
11	828	16.2	508	2	Q8BUA5
12	826.5	16.2	515	2	Q96R50
13	820.5	16.0	515	2	Q96R50
14	772	15.1	360	2	Q8N732
15	714.5	14.0	428	2	Q96P76
16	714	14.0	429	2	Q96LA6
17	651.5	12.7	509	2	Q91YK7
18	645.5	12.6	509	2	Q9EQY5
19	628	12.3	366	2	Q8N759
20	548	10.7	124	2	Q6UY46
21	545.5	10.7	255	2	Q9B216
22	543.5	10.6	154	2	Q8N733
23	537	10.5	343	2	Q8BY84
24	534.5	10.4	422	2	Q96P73
25	531	10.4	343	2	Q8RAY0
26	529.5	10.3	324	2	Q7TWH2
27	488.5	9.5	722	2	Q6G8N3
28	464.5	9.1	300	2	Q68SP0
29	448.5	8.8	426	2	Q6BA44
30	446.5	8.7	626	2	Q6DCH3
31	433	8.5	192	2	Q9B215

32	430.5	8.4	4071	2	Q6KDZ1
33	428.5	8.4	357	2	Q8SPW5
34	418.5	8.2	374	1	FCG1 HUMAN
35	416	8.1	4391	1	PGBM HUMAN
36	415	8.1	208	2	Q80WN3
37	402.5	7.9	372	2	Q7YQJ5
38	402.5	7.9	404	1	FCG1 MOUSE
39	398.5	7.8	5636	2	Q96RW7
40	397	7.8	144	2	Q9B214
41	396	7.7	330	2	Q8RI42
42	396	7.7	7962	2	Q10465
43	396	7.7	34350	2	Q8W242
44	383	7.5	738	2	P79390
45	375.5	7.3	434	2	Q6DN72

ALIGNMENTS

RESULT 1  
Q96RD9 PRELIMINARY; PRT; 977 AA.  
AC Q96RD9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE FC receptor-like protein 5.  
GN Names=FCRH5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;  
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;  
RT "Identification of a family of FC receptor homologs with preferential  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).  
DR HSSP: P12319; 1F2Q.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003598; Ig\_c2.  
DR SMART: PF00047; Ig; 8.  
DR SMART: SM00408; IGC2; 1.  
DR PROSITE: PS50835; IG\_LIKE; 8.  
KW Receptor.  
SQ SEQUENCE 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;

Query Match 100.0%; Score 5115; DB 2; Length 977;  
Best Local Similarity 99.9%; Pred. No. 5.2e-315;  
Matches 976; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVFQGERVLTCKGFRFSPQTKWYHR	60
Qy	61	YLKGETLRTPDNILSVQSGEYRCQAQSPVHLDFSSASLILQAPLSVFEGDSVV	120
Db	61	YLKGETLRTPDNILSVQSGEYRCQAQSPVHLDFSSASLILQAPLSVFEGDSVV	120
Qy	121	LRCAKAEVTLNNTIYKNDNLVLAFLNKRITDFHIFHACLKNDNGAYRCTGYKESCCPVSSNT	180
Db	121	LRCAKAEVTLNNTIYKNDNLVLAFLNKRITDFHIFHACLKNDNGAYRCTGYKESCCPVSSNT	180
Qy	181	VKIQVEPTRPVLRASSQPIISGNPVTTCTETQLSLERSDVLPRFRFRDDQTLGLGWS	240
Db	181	VKIQVEPTRPVLRASSQPIISGNPVTTCTETQLSLERSDVLPRFRFRDDQTLGLGWS	240
Qy	241	LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSRSMIQQVQIPASHPVLTLSPEKALNFE	300
Db	241	LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSRSMIQQVQIPASHPVLTLSPEKALNFE	300

DR PROSITE; PS50835; IG\_LIKE; 3.  
FT NON\_TER 1\_1  
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523B52CA CRC64;  
Query Match 40.9%; Score 2091; DB 2; Length 437;  
Best Local Similarity 99.8%; Pred. No. 4.2e-124;  
Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 573 PRAQAVVGDLELHCEAPRGSPPILYFVHEDVTLGSSSAPSGEASFNLSLTAHSGNY 632  
DB 33 PGAQAVVGDLELHCEAPRGSPPILYFVHEDVTLGSSSAPSGEASFNLSLTAHSGNY 92  
QY 633 SCANNGLVAQHSDDTISLSVIVPVSRLTFRAPRAQAVVGDLELHCEALRGSSPILY 692  
DB 93 SCANNGLVAQHSDDTISLSVIVPVSRLTFRAPRAQAVVGDLELHCEALRGSSPILY 152  
QY 693 FYHEDVTLGKISAPSGGASFNLSLTHSGIYSCADNGLAQRSEMTLKVAVPVSRLP 752  
DB 153 FYHEDVTLGKISAPSGGASFNLSLTHSGIYSCADNGLAQRSEMTLKVAVPVSRLP 212  
QY 753 VLTTRAPGTHAAVGDLELHCEALRGSPILYRFFHEDVTLGNRSSPSGGASLNLSLTA 812  
DB 213 VLTTRAPGTHAAVGDLELHCEALRGSPILYRFFHEDVTLGNRSSPSGGASLNLSLTA 272  
QY 813 HSGNYSCEADNGLAQRSEMTLKVAVPVSRLTFRAPRAQAVVGDLELHCEALRGSSPILY 872  
DB 273 HSGNYSCEADNGLAQRSEMTLKVAVPVSRLTFRAPRAQAVVGDLELHCEALRGSSPILY 332  
QY 873 LSRKAGKRPASDPARSFSDSDSQEPTVHNPVPAVEELQPVYTNANPRGENVYSEVRIIOE 932  
DB 333 LSRKAGKRPASDPARSFSDSDSQEPTVHNPVPAVEELQPVYTNANPRGENVYSEVRIIOE 392  
QY 933 KKHAVASDPRLHKNKSPILYSEVKVASTPVSGLFLASSAPHR 977  
DB 393 KKHAVASDPRLHKNKSPILYSEVKVASTPVSGLFLASSAPHR 437

RESULT 3  
Q96LA4 PRELIMINARY; PRT; 734 AA.  
ID Q96LA4  
AC Q96LA4; 19, Created  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 26, Last annotation update)  
DE Fc receptor-like protein 3.  
GN Name=FCRH3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;  
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;  
RT Identification of a family of Fc receptor homologs with preferential  
RT B cell expression.  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).  
DR EMBL; AY043466; AAK91779.1; -.  
DR HSSP; P12319; 1F2Q.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR002052; N6\_Mtase.  
DR Pfam; PF00047; ig; 4.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 6.  
DR PROSITE; PS00092; N6\_MTASE; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;  
Query Match 30.6%; Score 1563; DB 2; Length 734;  
Best Local Similarity 37.2%; Pred. No. 2.1e-90;  
Matches 365; Conservative 94; Mismatches 215; Indels 306; Gaps 13;

Qy	1	MLLWVILLVLPVSCQFARTPRPIIFLOPQWTVTFQGERVTLTCGRFRFYSPQ-KTKWYH	59
Db	1	MLLWVILLVLPVSCQFARTPRPIIFLOPQWTVTFQGERVTLTCGRFRFYSPQ-KTKWYH	60
Qy	60	RYLGEIILRETPDNTLLEVOESEGEYRCAQGSPLSSPVHLDPFSASILLOAPLSVPEGDSV	119
Db	61	---DEKLKIKHKDKI-QITEPGNYOCTKRSGSLSDAVHVEFSPDMLILLOALHPVPEGDV	116
Qy	120	VLRCRAKAEVTLNNTIYKXNDNVLAFLNKRDTPHIACILKONGAVRCTCYKESC---	CPV 176
Db	117	ILRCOGKDNKTHQKVYKQKQOLPNSYNLEKITYNSVSRDNSKVHCTAYRKFYILDIEV	176
Qy	177	SSNTVKIQVQEFTRPVLRASSFQPIGNNPVTLCCTQLSLSRSDVPLRFRFRDDQTGL	236
Db	177	TSKPLNIQVQLFLHPVLRASSSTIEGSPMTLCCTQLSPQRDPVQLQSLFRDSQTLG	236
Qy	237	LGWSISLNPFOITAMWSKDSGFVCKAAATPHSVISDSPRSMTQVQIPASHPVLTLSPEKA	296
Db	237	LGWSRSPRLQIPAMWTEDSGSVCEVETVTHSIKKRSLRSQIRVQ-----	281
Qy	297	LNFEGTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVRCEGASISFSLTTENSGNYCT	356
Db	282	-----	281
Qy	357	ADNGLGAKPSKAVLSVTVPVSHPVNLSSPBDLIFECAKVTLHCEAQRGSLFIYQFHH	416
Db	282	-----RVPVSNVNLEIRPTGGQLEGENMVLCISVAGSGTVTFVSWHK	324
Qy	417	ED--AALERRSANSAGGVAISFSLTAESHGNYCTADNGFGPQRKAVLSLTVPVSHPV	474
Db	325	EGRVRSLGRKT-----QRLSLAEHL-----	345
Qy	475	LTLSSAEALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSTPSVGRVSFSLTEG	534
Db	346	LTVKESDA-----	353
Qy	535	HSNGNYCTADNGFGPQRSEVVSFLTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSP	594
Db	354	--GRYCAADNVHSPILSTWIRVTVRIPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSP	411
Qy	595	PILYWFYHEDVTLGSSSAPSGGEASFNLSTLTAESHGNYSCNANGLVIAQHSOTISLVIV	654
Db	412	PILYRFYHEDVTLGNSSAPSGGASFNLSTLTAESHGNYSCDADNGLGAQHSRGVSLRVTV	471
Qy	655	PVSRPILTFRAPQAQVVGDLLELHCEALRGSSPILYWFYHEDVTLTKISAPSGGASFN	714
Db	472	PVSRPVLTLRAGAQAQVVGDLLELHCESLRGSPILYWFYHEDDTLGNISAHSGGASFN	531
Qy	715	LSLTTESHSIGYSCDADNGLAEQSRSEMTVLKAVPVSRPVLTLRAPGTHAAVGDLELHCE	774
Db	532	LSLTT-----	536
Qy	775	ALRGSPILYRFHEDVTLGNRSSPSGGASLNLSTLTAESHGNYSCDADNGLGAQSRSETV	834
Db	537	-----EHSNGNYSCDADNGLGAQHSKVTV	559
Qy	835	LYITGLTANRSGPATVAGGLISLAGAAGALLYCWLSRKAGRP-----	881
Db	560	LNVTGTSNRRTGLTAAGITGLVLSLVLAAALHLH---YAPARRKPGLSATGTSSHP	616
Qy	882	--ASDPARS-PSDSDSQSBTPYHNVPAWELQPVYTNANPRGENVYVSEVRIIEQKKCH	938
Db	617	SECQEPSSRRSRIDPQFTHSKPLAPMELEPMYSNANPGDSNPYISQIWSLQHTKNSA	676
Qy	939	ASDPRHLNKGSPIIYSEVK	958
Db	677	NCPMMHQHEELTVLYSELK	696

RESULT 4

Q96FP31

ID Q96FP31

PRELIMINARY:

PRT: 734 AA.

Q06P31;  
01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE SH2 domain-containing phosphatase anchor protein 2a.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Xu M.-J., Zhao R., Zhao Z.J.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RT EMBL; AF416901; AAL13290.1; -;  
DR HSPG; P12319; IP2Q.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig c2.  
DR InterPro; IPR002052; N6\_Mcase.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00835; IG\_LIKE; 6.  
DR PROSITE; PS00092; N6\_MTASE; UNKNOWN 1.  
SQ SEQUENCE 734 AA; 80855 MW; B341B73A35EC668 CRC64;

Query Match 30.5%; Score 1559; DB 2; Length 734;  
Best Local Similarity 37.1%; Pred. No. 3.8e-90;  
Matches 364; Conservative 94; Mismatches 216; Indels 306; Gaps 13;

Qy	1	MLLWVILLVLAPVSGQPARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPQ-KTKWYH	59
Db	1	MLLWLLLLILTPGREQSGVAPKAVLLLPWPSTAFKEKVALICSSISHSLAQDITYWH	60
Qy	60	RYLKGELRETPDNILEVOBSGEYRCOAQGLSSPVHLDFSASILTQAPLSVFEGDSV	119
Db	61	--DEKLKKIKHKI-QITEPGNYQCKTRGSSLSDAVHVEFSDWLILQALHPVFEDNV	116
Qy	120	VLCRKAAYETLVNTTYKNNDVLAFLNKRDFPHIACLKDNAGYRCTGYKESC--CPV	176
Db	117	ILRCQGKDNKNTHQVKYKDGKQLPNSYNLEKITVNSVRSDNSKYHTAYRKFIILDIEV	176
Qy	177	SNYVIKIQQEPTFRPVLRASSFPQISGNPNVITTCETOLSERSDVPLRFRFRDDOTLG	236
Db	177	TSKPLNIQVOELFLHPVLRASSFTPIEGSPMTLTCTQLSPORPDVQLQSLFRDSOTLG	236
Qy	237	LGSLSLSPNFOTAMWKSDGFYKCAATMPSVISDSPSRMWIOVIPASHPVLTLSPEKA	296
Db	237	LGWRSRPLQIPAWMTTSDGSVCWEVTVTHSIKKSLRSQIRVQ-----	281
Qy	297	LNFEGTKVTILHCETQEDSLRTLRYRFHEGVPLRHKSVCER GASISFSLTTENSGNYCYT	356
Db	282	-----	281
Qy	357	ADNLGAKPSKAVSLSVTPVPVSHPVNLNSPEDLIPEGKVTLHCRAGRQSLPILYQFH	416
Db	282	-----RVPSVNVLNLEIRPTGGQLIEGENNMVLICSVAQSGTGTFTSWHK	324
Qy	417	ED--AALERESANSAGGVAISFSLTAHSGNYCYTADNGFGPORSKAVSLSIIVPSHPV	474
Db	325	EGRVSLGRKT-----QRSLAEIHH-----V	345
Qy	475	LTLSSAEALTFFEGATVTLHCEVGQSQILYQFYHEDMPLWSSSTPSVGRVSFSLSLEG	534
Db	346	LTVKESDA-----	353
Qy	535	HSNGYYCTADNGFGPORSEVVSLFTVPVPSRPILTURVPAQA VGDLLLELHCEAPRGSP	594
Db	354	--GRYTCADNVHSPILSTWI RTVIRIPVSHPVLTTPRAPRAHTVWGDLLELHCESLRGSP	411
Qy	595	PILYWFHEDVTILGSSASPSCGEASFNLISLTAHSGNYSCEANGLVAQHSDTILSVIV	654
Db	412	PILYRFHEDVTILGNSSAPSGGGA FNLSLTASHSGNYSCDANGIGAQHSHGVLRVTV	471
Qy	655	PVSRPILTTPRAQAQVVGDLLELHCEALRGSSPILYFWFHYEDVTILGKISAPSGGGA SFN	714

Thu May 5 15:11:02 2005

Db 472 PVSREVLTLRPAQAQVVDLLEHCELSRSPFLLYFWFHEDDTLGNISAHSGGASFN 531  
 QY 715 LSLTTHSGIYSCDADNGLEAQRSEMTLVKVPVSRPVLTLRPAQTHAAVGDLELHCE 774  
 Db 532 LSLTT-----536  
 QY 775 ALRGSPLILYRFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSETVT 834  
 Db 537 -----EHSNGNYSCEADNGLGAQHSKVVT 559  
 QY 835 LYITGLTANRSGPFATGVAGLLSIAGLAAGALLYCWLRSKAGRP-----881  
 Db 560 LNVGTGSRNRTGLTAAGITGLVLSILVLAALHLLH---YARARRKPGGLSATGTSSHP 616  
 QY 882 --ASDPARS--PSDSQSEPTTHNVPAWELOPYNNANPRGENVYSEVRILIQEKKHAY 938  
 Db 617 SECQEPSSRRPRIDPQEPHKSPLAPMELEPMYSNVNPGDSNPYISQIWSIQHTKNSA 676  
 QY 939 ASDPRHLRNKSGPIIYSEVK 958  
 Db 677 NCPMMHQHEELIVLYSELK 696

## RESULT 5

Q8N6S2 PRELIMINARY; PRT; 742 AA.  
 AC Q8N6S2;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE FCRH3 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer T., Max S.I., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC028933; AAH28933.1; -;  
 DR HSSP; P12319; 1F2Q.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig C2.  
 DR InterPro; IPR002052; N6\_Mtase.  
 DR Pfam; PF00047; 19; 4.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_Like; 6.

DR PROSITE; PS00092; N6\_Mtase; UNKNOWN 1.  
 SQ SEQUENCE 742 AA; 81853 MW; B0650200E7CA19B8 CRC64;  
 Query Match 30.5%; Score 1559; DB 2; Length 742;  
 Best Local Similarity 37.1%; Pred. No. 3.9e-90; Indels 306; Gaps 13;  
 Matches 364; Conservative 94; Mismatches 216;  
 1 MLLWILLVLAVPSQFARTPRPIIFLQPPMTTTFQGERVLTCKGRFRFVSPQ-KTKWYH 59  
 1 MLLWILLVLITPGRQSGVAPKAVILLNPNPMTAFKGEKVALICSSISHSLAOGDTWYH 60  
 60 RYLKKEILRETDPNILEVOESGEYRCQAQSPSLSPVHLDFSSASLILQAPLSVFEQDSV 119  
 61 ---DEKLLIKHDKI-QITEPCNYQCKTSGSLSDAVHFEFSPDWLILQALHPVFEQDNV 116  
 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPFHIPLACLKNGAYRCTGYKESC---CPV 176  
 117 ILRCQKDNKNTKOKVYKDKQLPNSVNLKTIYNSVSRDNKSYKCYAKFYKFLDIEV 176  
 177 SSNTVKIQVQEPFTRFVLRASSFQIPISGNPVLITCETQLSLERSDPLRFFRDDQTLG 236  
 177 TSKPAINIQVELFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPDVLQFLFRDSQTLG 236  
 237 LGWSLSPFOITAMKSKDSGFYWCRAATMPHPSVISDSPRSMTQVQIPASHPVLTLSPKA 296  
 237 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ-----281  
 297 LNFEGTKVTLHCETQDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356  
 282 -----281  
 357 ADNGLGAKPKASVLSVTVPVSHPVNLSPEDLIFEGAKVTLHCEAORGSLPILYQFHH 416  
 282 -----RVFVSNVNLREIRPTGQGLIEGENWVLICSAVQSGGTVTFTSMHK 324  
 417 ED--AALERSANSAGGVAISFSLTAHSGNYCTADNGFGPQSPKAVLSLITVPSHV 474  
 325 EGRVRSRQKLT-----QRSLAEHL-----V 345  
 475 LTLSSAALTFEGATVTLHCEVORGSPQIILYQFYHEDMPLWSSSTSPVGRVSPSFLITEG 534  
 346 LTVKESDA-----353  
 535 HSGNYCTADNGFGPQSPSEVSVLFTVPVSRPILTLRVPRAQAVVGDLELHCEAPRGSP 594  
 354 --GRYCAADNVHSPILSTWIRVTRIPVSHPVLTPRAHTVVGDLLEHCELSRGSP 411  
 595 PLYWYFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQSHDITSLISVIV 654  
 412 PLYRPFYHEDVTLGNSSAPSGGASFNLSLTAHSGNYSCEADNGLGAQSHGSLRVTV 471  
 655 PVSRLTLFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFN 714  
 472 PVSRLTLFRAPRAQAVVGDLELHCELSRGSPFLYWFYHEDDTLGNISAHSGGASFN 531  
 715 LSLTTHSGIYSCDADNGLEAQRSEMTLVKVPVSRPVLTLRPAQTHAAVGDLELHCE 774  
 532 LSLTT-----536  
 775 ALRGSPLILYRFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSETVT 834  
 537 -----EHSNGNYSCEADNGLGAQHSKVVT 559  
 835 LYITGLTANRSGPFATGVAGLLSIAGLAAGALLYCWLRSKAGRP-----881  
 560 LNVGTGSRNRTGLTAAGITGLVLSILVLAALHLLH---YARARRKPGGLSATGTSSHP 616  
 882 --ASDPARS--PSDSQSEPTTHNVPAWELOPYNNANPRGENVYSEVRILIQEKKHAY 938  
 617 SECQEPSSRRPRIDPQEPHKSPLAPMELEPMYSNVNPGDSNPYISQIWSIQHTKNSA 676  
 939 ASDPRHLRNKSGPIIYSEVK 958



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Db 677 NCPMMHQHEBELTVLYSELK 696
RESULT 6
Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416903; AAL13292.1; -.
DR HSSP; P12319; IP2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 740 AA; 81440 MW; 038AF83A2909E46 CRC64;

Query Match 30.3%; Score 1549; DB 2; Length 740;
Best Local Similarity 37.0%; Pred. No. 1.7e-89;
Matches 365; Conservative 94; Mismatches 215; Indels 312; Gaps 14;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPO-KTKWYH 59
DB 1 MLLWILLVLTPREGQGVAPKAVLLNPNPSTAFKGEKVALICSSISHSLAQDITYWH 60
QY 60 RYLKKEILRTPDNILEVQESGEYRCQAQSGPLSSPVHLDFSSASLIQLAPLSVFEGDSV 119
DB 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLIQLALHPVFEQDNV 116
QY 120 VLRCRAKAEVTLNNTIYKNDVLAFLNKRDTFHI PHACLKNDGAYRCTGYKESG---CPV 176
DB 117 ILRCQCKDNKNTHKQVYKDGKQLPNSYNLEKITSVSRDNSKSYHCTAYRKFIYLDIEV 176
QY 177 SSNTVKIQVEPFRPVLRRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDDOTLG 236
DB 177 TSPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCTQLSPQRPDVLQQLSLFRSDQTLG 236
QY 237 LGWSLSPNFOITAMWSKDSGFYCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKA 296
DB 237 LGWSRSPRLQIPAWMTEDSGYCEVETVTHSIKRSLSRQIRVQ-----281
QY 297 LNFEQTKVTLHCETQEDSLTLRYFYHEGVPLRHKSVRRCRGASISFSLTENSNGNYCT 356
DB 282 -----281
QY 357 ADNGLGAKPKAVSLSVTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
DB 282 -----RVPVSNVNLRIPTGGQLIEGENKNVLICSVAAQSGSVTFVSMWK 324
QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPORSKAVSISITVPVSHPV 474
DB 325 EGRVSLGRKT-----QRLSLAEHL-----V 345
QY 475 LTSSABALTFEGATVTLHCEVQSGPILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
DB 346 LTVKESDA-----353
QY 535 HSGNYCYCTADNGFGPQSEVVSFLV-----TVPVSRPILTLRPRAQAVVGLLHCE 588
DB 354 --GRYYCAADNVHSPILSTLWIRVTRTLSPSPVPSHPVLTFRAPRAHTVVGDLLEHCE 411
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QY 589 APRGSPPILYFYHEDVTLGSSAPSGGEASFNLSTAEHSGNYSCSANNGLVAQHSDTI 648
DB 412 SLRGSPPILYFYHEDVTLGNSAPSGGGASFNLSLTAHSGNYSCDADNGLGAQSHGV 471
QY 649 SLSVIVPVSRIPLTFRAPRAQAVVGLLELHCEALRGSSPILYFYHEDVTLGKISAPSG 708
DB 472 SLRTVTPVSRPILTLRAPGAQAVVGLLELHCESLRGSFPILYFYHEDDTLGNISAHSG 531
QY 709 GGASFNLSTLTHSGIYSCDADNGLEAQRSEMVTLKVAVPVSRPVLTLRPGTHAAVGD 768
DB 532 GGASFNLSTL-----542
QY 769 LELHCEALRGSPILYFYHEDVTLGNRSPSGASLNLSTAEHSGNYSCDADNGLGAQ 828
DB 543 -----EHSNGYSCDADNGLGAQ 559
QY 829 RSETVTLITGLTANRSGPPATGVAGGLLSIAGLAAGALLIYCWLSRKAGRKP-----881
DB 560 HSKVVTLVNVTGTSRNRGTAAAGITGLVLISILVAAAAALLH---YARARRKPGGLSATG 616
QY 882 -----ASDPARS-PSDSDSOEPTVHNVPVWEELQPVVTNANPRGENVYVSEVRIQE 932
DB 617 TSSHSPSECOEPPSSRPRIPOETHSKPLAPMELEPMYSNVNPGDSNFIYQIOWSIQH 676
QY 933 KKHAVASDPRLHNRKSGPIIYSEVK 958
DB 677 TKSANCPMMHQHEBELTVLYSELK 702
RESULT 7
Q96P30 PRELIMINARY; PRT; 639 AA.
AC Q96P30
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416902; AAL13291.1; -.
DR HSSP; P12319; IP2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 639 AA; 63928 MW; DEAD7ADAE64CA984 CRC64;

Query Match 23.6%; Score 1205.5; DB 2; Length 639;
Best Local Similarity 31.2%; Pred. No. 7.5e-68;
Matches 305; Conservative 85; Mismatches 192; Indels 395; Gaps 14;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPO-KTKWYH 59
DB 1 MLLWILLVLTPREGQGVAPKAVLLNPNPSTAFKGEKVALICSSISHSLAQDITYWH 60
QY 60 RYLKKEILRTPDNILEVQESGEYRCQAQSGPLSSPVHLDFSSASLIQLAPLSVFEGDSV 119
DB 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLIQLALHPVFEQDNV 116
QY 120 VLRCRAKAEVTLNNTIYKNDVLAFLNKRDTFHI PHACLKNDGAYRCTGYKESCCPVSSN 179
DB 117 ILRCQCKDNKNTHKQVYKDGKQLPNSYNLEKITSVSRDNSKSYHCTAYRK-----168
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submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AY158090; AAC20873.1; -.  
HSP; P12319; IF2Q.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003598; Ig\_c2.  
Pfam; PF00047; Ig; 3.  
SMART; SM00408; IGC2; 2.  
PROSITE; PS50835; IG\_LIKE; 5.  
SEQUENCE 582 AA; 65248 MW; 44321E93FE9EDF06 CRC64;

Query Match  
20.9%; Score 1067; DB 2; Length 582;

Query Match: 15;  
Best Local Similarity 29.8%; Pred. No. 3.8e-59;  
Matches 282; Conservative 82; Mismatches 191; Indels 390; Gaps 15;

3 LMVILLVLPVSGQFARTPRPIIFIQPPWTTVFQGERVTLTCGFRFVSPQKTKWVHYL 62

1 MMLTLLVTPVNGQHEAAQQSVLSLQPPWTTFFRGEVVILTCYRFGFSVPKTKM?K-- 58

63 GKEILRETPD-----NILEVQSEGRKCAQGSFSSFLRDDIUSGRLA  
 :  
 59 -BYWKOTPGALVIKAHLTKHESGYWCADILLPSMHVNVEFSDFVLQAAPPVFE 117

117 DSVILCRKAÆVTLNN-TIVKNDNVLAFLNKRIDFHI PHACLKDNAGYRCTGYKESC-- 173

118 DSVVLCYAKKIEAETLTFYKDGKALT-LHQSELSIHANLKDNGYKCTSKKWSFG 176

174 CPVSNVTKIQVOEPPFTRPVLRASSFQIPISGNPVTLTCTETQISLERSDVLPRFFRRDDQ 233

177 SLYTSNTVGQVQGLFPRPLKARPSHELDGSEVLILCCQLQSHAKAGKPKNGKSTLRNKA  
234 TIIGHGWSI SPNEOITAMWSKDGGFYWCXKAATMPHSVISDSRPSWIQVQIPASHPVLTLSLP 293

237 LLGSGSRSEFHIPAIWTEESRRYYQCAETVNSQVRKQSTAFIPVQ----- 284

294 EKALNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGY 353

b 285 -----RASARQTHIIP----- 296  
-----HCEAORGSLPILYO 413

354 YCTADNGLGAKPKSAVLSLVFVSHFVLNDSSEEDLITDCAVLAZGEGVGEV  
297 ----- 296

414 FHEDAALERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSTVPVSH 473

b 297 ----- 296

474 VLTSSAEALTFEGATVTLHCFVQSGPQLLYQFYHEDPMLWSSSPVSGVRSFSFLTE 533

297 -----ASKLVFEGQLLELLNC SVKVGFGPLATSWIKGM  
534 CHSGNVYCTADNGFGPORSSEVLSLEVTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGS 593

330 ----- 329

594 PPILYWFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVI 653

db 330 -----LNEETKILKSS-----NAEFKIS----- 347  
330 -----LNEETKILKSS-----NAEFKIS----- 713

654 VPVSRPILITFRAPRAQAVVGGDLLLELHCEALRGSSPILWFIHEDVILGKALSAFVGGGSLA  
249 : OVNISD  
353

714 NLSLTTEHSGIYSCSEADNGLEAQRSEMVTLKVAVPVSRPVLTLPAGTHAAVGDLELHC 773

354 -----AGEYHCEATNSRRSFVSRAFPITIKYVPVSPVLTLSTGKTQALEGDLMTLHC 405

774 EALGSPILYRFFHEDVTLGNRSSPS-GGASINLSLTAEHSGNSYSCDANGLGARQSET 833

406 QSQRGSPCILYBFFYENVUSLGNSSILSGGGAIFNFMSIERGNIICIRAGNOLZKQJGZ  
933 VTHVITGHTANBSQPFATGVAGGLSITAGLAAGALLLYCWLKRYAGRKPPADPARSPDS 892

466 IRISFDMTKNSVPMAAGITVGLLI--MAVGVLFLYCFWFSRKGAGKPTSDSRNPDS 522

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QY 893 DSQPTVHNVPAMELOPVTYNNPRGENVYSEVRIIOEKKKHA 937
Db 523 EPOEPTYNNPACIELOPVYSN-EPE-ENVIYTEVRRTPQKHA 565

RESULT 9
Q68SN8 PRELIMINARY; PRT; 595 AA.
AC Q68SN8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FC receptor-like protein 3.
GN Name=FcRh3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RA PubMed=15302849;
RX Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;
RT "Differential B cell expression of mouse Fc receptor homologs.";
RL Int. Immunol. 16:1343-1353(2004).
DR EMBL; AY506558; AAS91578.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001595; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 4.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Receptor.
SQ SEQUENCE. 595 AA; 66619 MW; 6AEDB8E2F6AFACF CRC64;

Query Match 20.9%; Score 1067; DB 2; Length 595;
Best Local Similarity 29.8%; Pred. No. 4e-59;
Matches 282; Conservative 82; Mismatches 191; Indels 390; Gaps 15;

QY 3 LWILLVLAVPSGQFARTPRITLQPPWTVFQGERVTLTKGFRPYSPQKTKWVHYRL 62
Db 14 MWLLTLVTPVNGHEAAQSVLSQPPWTVFQGERVTLTKGFRPYSPQKTKWVHYRL 71
QY 63 GKILRETPD-----NILEVQSGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVPEG 116
Db 72 -RTVVTQTPGALVIKHTLVKHSGEYWCQADSLPSMHVNVFSEDFLVLPQAPVFE 130
QY 117 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRTDTHIPHACLKNDGAYRCTGYKESC-- 173
Db 131 DSVVLRCAKKGIEAEFLTYKDGKALT-LHQSELSIHLANKDNGQYKTSKKKWSFG 199
QY 174 CPVSSNTVKIQVEPPTPRVLRASSFQIPSGNPVTLTCETQLSLERSDPLRFRFRDDQ 233
Db 190 SLYTSNTGVQVQELFPRVLRARPSHPIDGSPVTLTCQQLSAQSDARLQCFERNLQ 249
QY 234 TLGLGWSLSPFOITAMWSKDSFGYCKAATMPSHVISDSFSPWIOVQIPASHPVLTSP 293
Db 250 LLGGGCSRSSEFHPAIWTBESRYQCAETVNSQVRKQSTAFIIPVQ----- 297
QY 294 EKALNPEGTKVTLHCETQEDSLRTLRFYHEGVPLRHKSVRCERGASISPSLATNSGNY 353
Db 298 -----RASARFQTHIP----- 309
QY 354 YCTADNGLGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGLPILYQ 413
Db 310 ----- 309
QY 414 FHEDAALERSANSAGGVAISFLTAHSGNYCYCTADNFGFPQRKAVSLSTIVPVSH 473
Db 310 ----- 309

474 VLTSSAALTFEGATVTLHCEVQSGPQILYQFYHEDMPLMSSSTFSGVGSFSLTE 533
310 -----ASKLVFEGQLLLNCSVKVGPGLKFSWYKDM----- 342
534 GHSGNYCYCTADNFGFPQRSEVSLFVTVPVSRPILTLRVPRQAQAVGDLLLEHCEAPRGS 593
343 ----- 342
594 PPILYWFYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCEANNGLVAQHSDTISLSVI 653
343 -----LNEETKLAKS-----NAEPKIS----- 360
654 VPVSRPILTFRAPQAQAVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGAS 713
361 -----QVNISD----- 366
714 NLSLTTEHSGIYSCADNGLAEQSRSEMTLVKAVPVSRPVLTLRAPGTHAAGVGLLELHC 773
367 -----AGEYHCEATNSRRSFVSRAPIITIKVPVSQPVLTILSTGKTQALEGLMTLHC 418
774 EALRGSPILYRFFHEDVTLGNRSSPS-GGASLNLSLTASHSGNYSCEADNGLCAQRSET 832
419 OSORGSPCILYEFYFNVSLSGNSILSGGAYFNFSMSTERSGNYCYTADNGLCAQSEA 478
833 VTLYITGLTANRSGPFATGVAGGLLSIAGLALGALLYCLWSRKAGRPASDPARSPSDS 892
479 IRISIDMTKNSRVPMAAGITVGLLI---MAVGVLFCYKFSRKAGGKPTSDSRNPSDS 535
893 DSQPTVHNVPAMELOPVTYNNPRGENVYSEVRIIOEKKKHA 937
536 EPOEPTYNNPACIELOPVYSN-EPE-ENVIYTEVRRTPQKHA 578

RESULT 10
Q96LAS PRELIMINARY; PRT; 508 AA.
AC Q96LAS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FC receptor-like protein 2 (FCRH2).
GN Name=FCRH2; ORFNames=UNQ9236;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of FC receptor homologs with preferential B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagta A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Gadowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2245-2270(2003).
DR EMBL; AY043465; AAK91778.1; -.
DR EMBL; AY358130; AAO88497.1; -.
DR HSSP; P12319; 1F2Q.
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DR Genew; HGNC:14875; SPAP1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30B0411B41EDC CRC64;

Query Match 18.2%; Score 931.5; DB 2; Length 508;
Best Local Similarity 29.6%; Pred. No. 1.2e-50;
Matches 254; Conservative 69; Mismatches 161; Indels 375; Gaps 13;

QY 104 SLILOAPLSVFEQSDVWLRCRAKAEVTLNNITYKNDN-VLAFLNKRTPDHPHACLKNDG 162
DB 19 SLTLVAPSSVFEQSDVILVKCQEQNKWKQAYHKDKELSVFKKFDLIQSAVLSDSG 78

QY 163 AYRC-TGYKESCCPVSSNTVKIQVEPFRPVLRASSQPTSGNPVTLTCTQLSLERSD 221
DB 79 NYFCSTKGQLFMDKTSNTVKIKVQELFORPVLTAASSQPIEGGVPVSLKCTETRLSPQLD 138

QY 222 VPLRFFRRDDTLGLGWSLSPNFQITAMWSKDSGYWCKAATMPHSVISDSPRSWIQVQ 281
DB 139 VOLOQCFRQNLVGGWSSSELPQLSAVWSEDTGSYCKAETVTHIRKQSLQSIHQV 198

QY 282 IPASHPVLTLSPEKALNFEGTKVTLHCETOEDSLRTLYRFFYHGVPLRHKSVCERGASI 341
DB 199 ----- 198

QY 342 SFLSTTENGNYCTADNGLGAKFSKAVLSVTVPVSHVPLNLSSPEDLIFEGAKVTLHC 401
DB 199 -----RIPISNVSLERAPCGQVTEGQKLLILC 226

QY 402 EAQSGSLPILYQPHHEDALERRSANSAGGVA-ISFSLTAHSGNYCTADNGFGPQSRK 460
DB 227 SV-----AGGTGNVTFSWYREATG-----TSMGKKTOR 254

QY 461 AVLSITVPVSHVPLTLSSAELTFEGATVTLHCEVQSGSPQILYQFYHEDPLWSSSFP 520
DB 255 SLSAELRIP----- 263

QY 521 SVGRVSFSLTECHSGNYCTADNGFGPQSRSEVSLFTVPVSRPILTLRVPRAQAVVG 580
DB 264 -----AVKESDAGKYCRADNGHVPQKVNIPVSRPVLTLRSPGAQAVG 314

QY 581 DLLELCEALRGPSPILYFYHEDVTLGSSAPSGGEAFNLISLTAHSGNYSCAANNGL 640
DB 315 DLLELCEALRGPSPILYFYHEDVTLGSSAPSGGEAFNLISLTAHSGNYSCAANNGL 374

QY 641 VAQHSDTLSLVIPVSRPILTPRAPAAQAVGDLLELHCEALRGSSPILYFYHEDVTL 700
DB 375 GAQCSEA-----VPVS----- 385

QY 701 GKISAPSGGASFNLSLTTESHSIGYSCADNGLEAQRSEWTLKAVPVRPVLTLRAPG 760
DB 386 -----ISGPDG-----YRDLMT----- 398

QY 761 THAAVGDLELHCEALRGPSPILYFYHEDVTLGNRSPSGASLNLTLTAHSGNYSC 820
DB 399 ----- 398

QY 821 ADNGLGAQRSEVTLTYITGLTANRSGPFATGVAGGLLSIAGLAAGALLYCWLSRKAGR 880
DB 399 -----AGVLNGLFGLVGTGVALLLYALPFIKISGES 429

QY 881 PASDPARPSDSQSEPTVHN-VPWELOPVTYTNANRGENVNVYSEVRIITQEKKKHAVA 939
DB 430 SATNEPRGASRNPQEFYTSSTPDMEELQPVYVGVSDVDVYVSQVSMQCFE---SSA 487

QY 940 SDPRHLRNKGPSIYSEVK 958
DB 488 NIRTLENKDSQVITYSSVK 506
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GN Name=FCRH4;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression."
RT Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).
DR EMBL; AF397452; AAK93970.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1 360
SQ SEQUENCE 360 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;

Query Match 16.0%; Score 820.5; DB 2; Length 515;
Best Local Similarity 43.3%; Pred. No. 1.3e-43;
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;

QY 1 MLLWVILLVLPVSGQFARTPRPIIQLQPPWTTVFOGERVTLTCKGFYSPQTKWYHR 60
DB 1 MLLWASLLAFVCGGQAAAHKVI SVHPWTTTFKGERVTLTCKGFQYATEKTTWYHR 60
QY 61 YLGEKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 HWGKLTLPFGNTLEVRSGLYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
QY 121 LRCRAKAEVTLNNTIYK-NDNVLAFLNKRDTDFHPACLKNGAYRCTGYKSCCPVSSN 179
DB 121 LRCHRRRKEKLTAVKYTWNGNLSISNKSNDLLIPQASSNNNGYRCIGYGDNDVFLN 180
QY 180 TVKIQVQPPFTRPVLRASSFQIPISGNPVTLTCTQSLERSDVLPRFRDRDQTLGLW 239
DB 181 FKIKIQELFPHPELKATDSQTEGNSVNLSCETQLPERSDTPLFHNFRRDGEVILSDW 240
QY 240 SLSPNFQITAMWSKDSGYWCAATMPSHVSIDSPRSWIOVO-IPASHPVLTLSPEKALN 298
DB 241 STYPELQPLTVWRENSGSGYWCAGETVRGNHHKSPSLQIHVQIPVSGVILETQPSGQA 300
QY 299 FEGTKVTLHCETQEDSLRTLVRFYHEGV--PLRHKSVCRCGASISFSLTTSNGNYCT 356
DB 301 VEGEMLVLCVSAEGTGTTFSHREDMQESLGRKTRSLRAELPAIRQSHAGGYCT 360
QY 357 ADNGLGAKPSKAVSLVTVVPSVHVLNLSPEDLIFEGA-----KVTLHCEAQ 404
DB 361 ADNLSYG--PVQSMVLNVTRETP-----GNRDGLVAAGATGGLLSALLAVALLFHCWRR 413
QY 405 RCS 407
DB 414 RKS 416

RESULT 14
Q8N732 PRELIMINARY; PRT; 360 AA.
ID Q8N732
AC Q8N732;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE D3801G22.1 (Novel immunoglobulin domain protein similar to
DE immunoglobulin receptors) (Fragment).
DE Names=DJ801G22.1;
GN Homo sapiens (Human)
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP Bagguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AL135929; CAB92753.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1 360
SQ SEQUENCE 360 AA; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match 15.1%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred. No. 9.5e-41;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIFLQPPWTTVFOGERVTLTCKGFYSPQTKWYHRYLKGKILRETPDNILEVOESG 81
DB 4 KPVISVHPWTTTFKGERVTLTCKGFQYATEKTTWYHRYWGEKLTLPFGNTLEVRSG 63
QY 82 EYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVVLRCPAKAEVTLNNTIYK-NDN 140
DB 64 LYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVVLRCPAKAEVTLNNTIYK-NDN 123
QY 141 VLAFLNKRDTDFHPACLKNGAYRCTGYKSCCPVSSNTVKIQVQPPFTRPVLRASSFQ 200
DB 124 ILSISNKSNDLLIPQASSNNNGYRCIGYGDNDVFRSNEFKIKIQELFPHPELKATDSQ 183
QY 201 PISGNPVTLTCTQSLERSDVLPRFRDRDQTLGLWLSLSPNFQITAMWSKDSGYWCA 260
DB 184 PTEGNSVNLSCETQLPERSDTPLFHNFRRDGEVILSDWSTYPELQPLTVWRENSGSGY 243
QY 261 KAATMPSHVSIDSPRSWIOVO-IPASHPVLTLSPEKALNFEKTKVTLHCETQEDSLRTLY 319
DB 244 GAETVRGNHHKSPSLQIHVQIPVSGVILETQPSGQAVEGEMLVLCVSAEGTGTTF 303
QY 320 RPYHEGV--PLRHKSVCRCGASISFSLTTSNGNYCTADNGLGAKPSKAVSLVTV 375
DB 304 SHWREDMQESLGRKTRSLRAELPAIRQSHAGGYCTADNSYG--PVQSMVLNVT 359

RESULT 15
Q96PJ6 PRELIMINARY; PRT; 428 AA.
ID Q96PJ6
AC Q96PJ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IFGP1.
OS Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guselnikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RT leukocyte FcR, gp42 and PECAM-1."
RT Immunogenetics 54:87-95 (2002).
RL EMBL; AF329488; AAL23898.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 3.

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SQ	SEQUENCE	428 AA; 46865 MW; F20BA31110BBC7828 CRC64;
	Query Match	14.0%; Score 714.5; DB 2; Length 428;
	Best Local Similarity	26.6%; Pred. No. 5.2e-37;
	Matches 207; Conservative	45; Mismatches 152; Indels 373; Gaps 9
Qy	188 PFTRPV---LRASSFQPIGSGNPVTLTCTQTLSLERSDVPLRFRPRDDQTGLGNSLSPN	244
Db		
Db	12 PLCEPABLFLLTASPSHPTEGSPVTLTKMPF-LQSSDAQFOCFRFRDTRALGPGWSSSPK	70
Qy	245 FQITAMMSKDSGFYCKCAATMPHSVIDSPPRSWIQVQIPASHPVLTLSPKALNPEGTKV	304
Db		
Db	71 LQIAAMNKBEDTGSYWCBAQTWASKVLR-SRSQINV-----	105
Qy	305 TLHCETOEDSLRILRYFHEGVPRLHKSVRCERGASISFSLTTENSGNYCTADNGLGAK	366
Db		
Db	106 -----HR-----	107
Qy	365 PSKAVLSLVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAALERR	424
Db		
Db	108 -----VPVADVSLTQPPGGQVMEGRDLVLI CSVAMGTGDIPLFWYKGAVGLNLQ	157
Qy	425 SANSAGGVAISFSLTAHSGNYCTADNGFGQRSKAVSLSIYVPVSHPVLTLSAEALT	484
Db		
Db	158 SKTOR-----SLTAAY-----	168
Qy	485 FEGATVTLHCEVQRGSPQLLYQFYHEDMPLSSSTPSPVGRVSPFSLTEHSGNYCYCTAD	544
Db		
Db	169 -----BIP-----SVRESDAEQYCYVAE	186
Qy	545 NGFGPQRSEVVLSLPTVPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWFYHED	604
Db		
Db	187 NGYGSPSGLVSIYTRIPVSRPILMLRAPQAQAVEDVLELHCEALRGSPPILYWFYHED	246
Qy	605 VTIGSSAPSGGGEASFNLSTLAHSGNYSCANNGLVAQHSDTISLSVIVPVSRIPLTFR	664
Db		
Db	247 ITLGRSAPSGGGASFNLSTEEHSGNYSCAN-----	279
Qy	665 APRAQAVVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSTLTHESGI	724
Db		
Db	280 -----	279
Qy	725 YSCADNGLCEAQRSEMVTLKVAVPVSRLPVLTLRAPGTHAAVGDLLLEHCEALRGSPILTY	784
Db		
Db	280 -----	279
Qy	785 RPFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCADNGLCAQRSETVTLTYITGLTANR	844
Db		
Db	280 -----NLGPAQRSEAVTLNFTVPTGAR	301
Qy	845 SGPFATGVAGGLLSIAGLAAGALLYCWLSRKAGRKCPASDPARSPSDSDSEPTVYHNVPA	904
Db		
Db	302 SNHLTSGVIEGLSLTLGPAIVALLFCYGLKKGIRRSARDPLRSLPPLPQEFYLYNSPT	361
Qy	905 WEELOPVYTANPGENVNVYSEVRIIQKKKHAVASDPRLHNRKSGSPIIYSEKVAS	961
Db		
Db	362 PGLOQPTIYENNVVSGDEVYSLAYNGPQESVAETLGTTHMEDKVSLDIYGLRLKAN	418

Search completed: May 4, 2005, 11:38:08  
Job time : 139.777 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 97.8093 Seconds  
(without alignments)  
3001.261 Million cell updates/sec

Title: US-09-724-254A-44  
Perfect score: 3993  
Sequence: 1 MLWVILLVLAPVSGQFART.....MVLKVGAEWALPTSSTSEN 759

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3993	100.0	759	4 AAB82313	Aab82313 Human imm
2	3993	100.0	759	7 ADM35235	Adm35235 Human LY1
3	3923	98.2	977	4 AAB82315	Aab82315 Human imm
4	3923	98.2	977	7 ADM35237	Adm35237 Human LY1
5	3916	98.1	977	6 ABP97215	Abp97215 Tumour-as
6	3720	93.2	875	8 ABM82476	Abm82476 Human dia
7	3487	87.3	837	8 ABM82477	Abm82477 Human dia
8	2962	74.2	592	4 AAB82314	Aab82314 Human imm
9	2962	74.2	592	7 ADM35236	Adm35236 Human LY1
10	1419.5	35.5	582	6 ABU99155	Abu99155 Novel hum
11	1419.5	35.5	582	8 ADM33875	Adm33875 Human NOV
12	1417.5	35.5	707	7 ADM06089	Adm06089 Human pro
13	1417.5	35.5	734	4 AAB82316	Aab82316 Human imm
14	1417.5	35.5	734	7 ADM35238	Adm35238 Human LY1
15	1417.5	35.5	750	8 ABM84916	Abm84916 Human dia
16	1415	35.4	733	8 ADL06557	Adl06557 Human tum
17	1400	35.1	727	6 ABM84668	Abm84668 Human SEC
18	1374.5	34.4	554	7 ADF74336	Adf74336 Extracell
19	1374.5	34.4	717	7 ADF74337	Adf74337 Human FCR
20	1374.5	34.4	717	7 ADF74318	Adf74318 Human FCR
21	1287.5	32.2	718	8 ABM84917	Abm84917 Human dia
22	1255	31.4	707	8 ABM84918	Abm84918 Human dia
23	1120	28.0	222	5 ABP69283	Abp69283 Human pol
24	1064	26.6	639	7 ADJ70604	Adj70604 Human hea
25	1064	26.6	655	8 ABM84920	Abm84920 Human dia

26	1012.5	25.4	641	8 ABM84919	Abm84919 Human dia
27	900	22.5	181	5 ABP51264	Abp51264 Human MDD
28	900	22.5	181	5 ABP51409	Abp51409 Human MDD
29	889.5	22.3	570	7 ADF74389	Adf74389 Murine FC
30	889	22.3	468	7 ADF74391	Adf74391 Extracell
31	884.5	22.2	327	5 ABP63021	Abp63021 Human pol
32	883	22.1	470	7 ADL22727	Adl22727 Human dis
33	871.5	21.8	421	6 ABU99156	Abu99156 Novel hum
34	871.5	21.8	421	6 ABU99157	Abu99157 Novel hum
35	871.5	21.8	421	8 ADM93877	Adm93877 Human NOV
36	868.5	21.8	508	4 AAB82317	Aab82317 Human imm
37	868.5	21.8	508	7 ADM35239	Adm35239 Human LY1
38	868.5	21.8	508	7 ADM35264	Adm35264 Human LY1
39	868.5	21.8	508	8 ADF89715	Adf89715 Human can
40	868.5	21.8	508	8 ADL06539	Adl06539 Human tum
41	864.5	21.7	445	7 ADM35268	Adm35268 Human LY1
42	864.5	21.7	489	7 ADF74316	Adf74316 Human FCR
43	858.5	21.5	380	7 ADF74334	Adf74334 Extracell
44	851.5	21.3	421	6 ABU99158	Abu99158 Novel hum
45	851.5	21.3	421	8 ADM93881	Adm93881 Human NOV

ALIGNMENTS

RESULT 1  
AAB82313  
ID AAB82313 standard; protein; 759 AA.  
XX AAB82313;  
AC AAB82313;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE Human immunoglobulin receptor isoform IRTA2a.  
XX  
KW Immunoglobulin superfamily receptor translocation associated; IRTA;  
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;  
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.  
XX  
OS Homo sapiens.

Key Peptide Location/Qualifiers  
1..15  
/label= signal\_peptide  
16..759  
/label= Mature\_protein  
FT Modified-site 132..134  
/note= "Asn is N-glycosylated"  
FT Modified-site 383..385  
/note= "Asn is N-glycosylated"  
FT Modified-site 621..623  
/note= "Asn is N-glycosylated"  
FT Modified-site 631..633  
/note= "Asn is N-glycosylated"  
FT Modified-site 714..716  
/note= "Asn is N-glycosylated"

W0200138490-A2.

31-MAY-2001.

28-NOV-2000; 2000WO-US032403.

29-NOV-1999; 99US-0168151P.

(UYCO ) UNIV COLUMBIA NEW YORK.

Dalla-Favera R;

WPI; 2001-355921/37.

N-PSDB; AAF30950.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor

Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at residue 746 and extends for a further 231 residues. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 759 AA;

Query Match 100.0%; Score 3993; DB 4; Length 759;  
Best Local Similarity 100.0%; Pred. No. 6.5e-248;  
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60  
QY 61 YLGEKILRETDPNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120  
Db 61 YLGEKILRETDPNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120  
QY 121 LRCRAKAEVTLNTIYKNDNVLAFLNKRTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNTIYKNDNVLAFLNKRTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVEPFTTRVLRASSFQPIGPNVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240  
Db 181 VKIQVEPFTTRVLRASSFQPIGPNVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240  
QY 241 LSPNFQITAMWKGSGFWCKAATWPHSVISDSRSMVQVOIPASHPVLTLSPEKALNFE 300  
Db 241 LSPNFQITAMWKGSGFWCKAATWPHSVISDSRSMVQVOIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETQDSLTLYRFRYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCTADNG 360  
Db 301 GTKVTLHCETQDSLTLYRFRYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSSPDLIPEGAKVILHCEAQRGSPILYQFHEDAA 420  
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPDLIPEGAKVILHCEAQRGSPILYQFHEDAA 420  
QY 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGQFQRKAVSLSITVPSHPVLTLSA 480  
Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGQFQRKAVSLSITVPSHPVLTLSA 480

QY 481 EALTREGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPVSFVSFSLTEGHSGNY 540  
Db 481 EALTREGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPVSFVSFSLTEGHSGNY 540  
QY 541 CTADNGFGQFQRSEVSVSLFVTVPVSRPILTLRVPRAQAVGDLLELHCEAPRGSPILYWF 600  
Db 541 CTADNGFGQFQRSEVSVSLFVTVPVSRPILTLRVPRAQAVGDLLELHCEAPRGSPILYWF 600  
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660  
Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660  
QY 661 LTRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTFE 720  
Db 661 LTRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTFE 720  
QY 721 HSGIYSCADNGLAEARSEMVTILKVAGEWALPTSSTSEN 759  
Db 721 HSGIYSCADNGLAEARSEMVTILKVAGEWALPTSSTSEN 759

RESULT 2  
ADM35235  
ID ADM35235 standard; protein; 759 AA.  
AC ADM35235;  
XX 03-JUN-2004 (first entry)  
DT Human LY448P cancer related protein for cancer detection method.  
DE cytostatic; T-cell vaccine; detection; cancer;  
KW chronic lymphocytic leukemia.  
XX Homo sapiens.  
XX WO2003077836-A2.  
PD 25-SEP-2003.  
XX 06-NOV-2002; 2002WO-US035728.  
XX 06-NOV-2001; 2001US-00040862.  
PR 23-MAY-2002; 2002US-00154884.  
XX (CORI-) CORIXA CORP.  
PA Gaiger A, Algate PA, Mannion J, Retter M;  
PI WPI; 2003-756941/71.  
XX  
DR Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.  
PT  
PT Disclosure; SEQ ID NO 10460; 419pp; English.  
XX  
XX The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicant has identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a protein used in the method of the invention.



CC nucleic acids and proteins, and antibodies directed to epitopes of IRTA  
CC proteins. Methods are claimed for: detecting a B cell malignancy  
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule  
CC that specifically hybridizes with a unique sequence of human IRTA1-5; and  
CC treating a subject having a B cell cancer by administering an anti-IRTA  
CC antibody or an antisense oligonucleotide that specifically hybridizes to  
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.  
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
CC Hodgkin's lymphoma  
XX  
XX  
Sequence 977 AA;

Query Match 98.2%; Score 3923; DB 4; Length 977;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSFQKTKWYHR 60

QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120  
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLGWS 240  
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLGWS 240

QY 241 LSPNFQITAMWSKDSGYKCAATMPSHVSIDSFRSWIQVOIPASHPVLTLSPEKALNPE 300  
DB 241 LSPNFQITAMWSKDSGYKCAATMPSHVSIDSFRSWIQVOIPASHPVLTLSPEKALNPE 300

QY 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360  
DB 301 GTKVTLCETQEDSLRTLRYFYHGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

QY 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVVSFSLTEGHSNYY 540  
DB 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVVSFSLTEGHSNYY 540

QY 541 CTADNGFGQRSEVSVLSFVTPVSPILTLRVPRAAQVVGDLLEHCEAPRGSPIILYWF 600  
DB 541 CTADNGFGQRSEVSVLSFVTPVSPILTLRVPRAAQVVGDLLEHCEAPRGSPIILYWF 600

QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660  
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660

QY 661 LTFRAPRAQAVVGDLLEHCEALRGSSPLLYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
DB 661 LTFRAPRAQAVVGDLLEHCEALRGSSPLLYWFYHEDVTLGKISAPSGGASFNLSLTTE 720

QY 721 HSGIYSCEADNGLAQORSEMWTLKVA 746  
DB 721 HSGIYSCEADNGLAQORSEMWTLKVA 746

RESULT 4  
ADM35237  
ID ADM35237 standard; protein; 977 AA.  
XX  
AC ADM35237;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
Human LY1448P cancer related protein for cancer detection method.  
XX  
cytostatic; T-cell vaccine; detection; cancer;  
XX  
chronic lymphocytic leukemia.  
XX  
Homo sapiens.  
XX  
WC2003077836-A2.  
XX  
25-SEP-2003.  
XX  
06-NOV-2002; 2002WO-US035728.  
XX  
06-NOV-2001; 2001US-00040862.  
XX  
23-MAY-2002; 2002US-00154884.  
XX  
(CORI-) CORIXA CORP.  
XX  
Gaiger A, Algate PA, Mannion J, Retter M;  
XX  
WPI; 2003-756941/71.  
XX  
Detecting cancer in a patient comprises contacting a biological sample  
XX  
from the patient with a binding agent that binds to a cancer-associated  
XX  
polypeptide and comparing the amount of polypeptide to a predetermined  
XX  
cutoff value.  
XX  
Disclosure; SEQ ID NO 10462; 419pp; English.  
XX  
The invention relates to a method of detecting (M1) cancer in a patient  
XX  
by: (i) contacting a biological sample from the patient with an agent  
XX  
that binds to any of three polypeptides given in the specification; (ii)  
XX  
detecting in a sample an amount of the peptide that binds to the binding  
XX  
agent; and (iii) comparing the amount of polypeptide present in the  
XX  
patient's sample to a predetermined cutoff value. The specification also  
XX  
discloses a separate method for detecting (M2) cancer in a patient by a  
XX  
method similar to M1, except that the detection agent is an  
XX  
oligonucleotide that binds to any of three polynucleotides given in the  
XX  
specification. M1 and M2 are useful for detecting the presence of cancer  
XX  
in a patient, especially chronic lymphocytic leukemia. The applicants  
XX  
have identified specific human polypeptides overexpressed in one or more  
XX  
types of hematological malignancies. This sequence corresponds to a  
XX  
protein used in the method of the invention.

Sequence 977 AA;  
Query Match 98.2%; Score 3923; DB 7; Length 977;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSFQKTKWYHR 60

QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120  
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDHPHACLDKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLGWS 240  
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLGWS 240

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Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Dy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Dy 301 GTKVTLCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSILPILYQPHHEDAA 420
Dy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSILPILYQPHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Dy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Dy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Qy 541 CTADNGFGPQRSEVSVLFTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
Dy 541 CTADNGFGPQRSEVSVLFTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
Qy 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Dy 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Qy 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Dy 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Qy 721 HSGIYSCADNGLAQRSEMWTLKVA 746
Dy 721 HSGIYSCADNGLAQRSEMWTLKVA 746

RESULT 5
ABP97215
ID ABP97215 standard; protein; 977 AA.
XX
AC ABP97215;
XX
XX 01-JUL-2003 (first entry)
XX
XX Tumour-associated antigenic target protein TAT374 SEQ ID NO:97.
XX
XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
XX
XX Homo sapiens.
XX
XX W02003024392-A2.
XX
XX 27-MAR-2003.
XX
XX 11-SEP-2002; 2002WO-US028859.
XX
XX 18-SEP-2001; 2001US-0323268P.
XX
XX 19-OCT-2001; 2001US-0339227P.
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XX 07-NOV-2001; 2001US-0336827P.
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XX 20-NOV-2001; 2001US-0331906P.
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XX 02-JAN-2002; 2002US-0345444P.
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XX 03-APR-2002; 2002US-0369724P.
XX
XX 19-AUG-2002; 2002US-0404809P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Frantz G. Hillan KJ, Phillips HS, Polakis P, Spencer SD;
XX
XX Williams PM, Wu TD, Zhang Z;
XX
XX WPI; 2003-354551/33.
```

```
DR N-PSDB; ACC49533.
XX
XX New antibodies against tumor-associated antigenic target polypeptide,
XX useful for treating or diagnosing tumors or cancers in mammals e.g.
XX prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
XX carcinomas.
XX
XX Claim 2; Fig 97; 285pp; English.
XX
XX ACC49493 to ACC49552 encode the human tumour-associated antigenic target
XX (TAT) proteins given in ABP97175 to ABP97234. The present invention
XX describes an isolated antibody that binds to a polypeptide having at
XX least 80 % sequence identity to any of the 60 150-800 residue amino acid
XX sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
XX its associated signal peptide, encoded by any of the 60 2000-3000 base
XX pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
XX cytostatic activity. The antibody can be used for treating or diagnosing
XX tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
XX cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
XX cell carcinomas, or thyroid cancer
XX
XX SQ Sequence 977 AA;
XX
XX Query Match 98.1%; Score 3916; DB 6; Length 977;
XX Best Local Similarity 99.9%; Pred. No. 8e-243;
XX Matches 745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1 MLWLWILLVLAPVSGOFARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPQTKWYHR 60
Dy 1 MLWLWILLVLAPVSGOFARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPQTKWYHR 60
Qy 61 YLCKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLIILQAPLSVEGDSVV 120
Dy 61 YLCKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLIILQAPLSVEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
Dy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLTCTQLSLERSDVPILRFFRDDDTLGLGWS 240
Dy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLTCTQLSLERSDVPILRFFRDDDTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Dy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Dy 301 GTKVTLCETQEDSLRTLRYFVHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSILPILYQPHHEDAA 420
Dy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSILPILYQPHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Dy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Dy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Qy 541 CTADNGFGPQRSEVSVLFTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
Dy 541 CTADNGFGPQRSEVSVLFTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
Qy 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Dy 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Qy 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Dy 661 LTRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
```

661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720

721 HSGIYSCDADNGLEAQRSEMTLKVA 746

721 HSGIYSCDADNGPEAQRSEMTLKVA 746

RESULT 6

ABM82476  
ID ABM82476 standard; protein; 875 AA.

AC ABM82476;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pprotein SEQ ID NO:2725.

DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

PD 12-SEP-2003; 2003WO-US028227.

PF 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
XX Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patry S, Shi X, Suarez CJ;  
XX WPI; 2004-329368/30.  
DR N-PSDB; ACN41128.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
DR in diagnosing a condition, disease or disorder associated with human  
DR molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
XX selected from one of the 2722 sequences defined in the specification. A  
XX polynucleotide of the invention may have a use in gene therapy. The human  
XX polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be  
XX used to diagnose a particular condition, disease or disorder associated  
XX with human molecules, e.g. cell proliferative disorders.  
XX autoimmune/inflammatory disorder, developmental disorder, endocrine  
XX disorder, neurological disorders, gastrointestinal disorders, or  
XX infections caused by virus, bacteria, fungi or parasite. The dithp  
XX molecules may also be used in genetic mapping, in identifying individuals  
XX from minute biological samples, in detecting single nucleotide  
XX polymorphisms, as molecular weight markers, and for somatic or germline  
XX gene therapy. The present sequence represents a dithp protein of the  
XX invention. Note: The sequence data for this patent is not represented in  
XX the printed specification, but was obtained in electronic format directly  
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 875 AA;

Query Match 93.2%; Score 3720; DB 8; Length 875;

Best Local Similarity 95.6%; Pred. No. 2.7e-230;

Matches 715; Conservative 7; Mismatches 14; Indels 12; Gaps 3;

QY 1 MLLWVILLVLA PVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSPOKTKWYHR 60  
DB 1 MLLWVILLVLA PVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSPOKTKWYHR 60  
QY 61 YLGEKILRETDPNILEVQESGEYRCAQGSPLSSPVHLDPFSSASLILQAPLSVFEQDSV 120  
DB 61 YLGEKILRETDPNILEVQESGEYRCAQGSPLSSPVHLDPFSSASLILQAPLSVFEQDSV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRITDFHPHACLKXNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRITDFHPHACLKXNGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS 240  
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS 240  
QY 241 LSPNFOITAMWSKDSGFYWCKAATMHSVISTDSPRWIOVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFOITAMWSKDSGFYWCKAATMHSVISTDSPRWIOVQIPASHPVLTLSPEKALNFE 300  
QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360  
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVLSLVTVPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGLPILYQPHHEDAA 420  
DB 361 LGAKPSKAVLSLVTVPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGLPILYQPHHEDAA 420  
QY 421 LERRSANSAGVAISFSLTAEHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSA 480  
DB 421 LERRSANSAGVAISFSLTAEHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSA 480  
QY 481 EALTFEAGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540  
DB 481 EALTFEAGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540  
QY 541 CTADNGFGPQRSSEVSLF-VTVPVSRPILTLRVPRAAVVGDLLELHCEAPRGSPPIIYW 599  
DB 541 CTADNGFGPQRSSEVSLF-VTVPVSRPILTLRVPRAAVVGDLLELHCEAPRGSPPIIYW 600  
QY 600 FYHEDVTLGSSAPSGGEASFNLSITAEHSGNYSCAANNGLVAQHSDTISLSVTPVSRP 659  
DB 601 FYHEDVTLGSSAPSGGEASFNLSITAEHSGNYSCAANNGLVAQHSDTISLSVTPVSRP 660  
QY 660 ILTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 719  
DB 661 ILTFR-----LLELHCEALRGSPILYWFYHEDVTLGNRSPS-GGASLNLSTA 709  
QY 720 EHSIGYSCDADNGLEAQRSEMTLKVA 747  
DB 710 EHSIGYSCDADNGLEAQRSEMTLKVA 737

RESULT 7

ABM82477  
ID ABM82477 standard; protein; 837 AA.

AC ABM82477;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pprotein SEQ ID NO:2726.

DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

PD 12-SEP-2003; 2003WO-US028227.





Claim 3; Fig 18B-1-18B-2; 72pp; English.

PS The present sequence is that of the novel human immunoglobulin receptor,  
XX immunoglobulin superfamily receptor translocation associated protein  
CC isoform 2b (IRTA2b), an Fc receptor involved in the pathogenesis of  
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal  
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma  
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding  
CC members of a novel subfamily of related receptors within the  
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA  
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).  
CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at  
CC residue 560, extending for a further 32 residues, whose hydrophobicity  
CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes  
CC display a specific pattern of expression in mature B cells. IRTA2 is  
CC expressed in GC centrocytes and in perifollicular cells, which may  
CC include immunoblasts and memory cells. The invention provides IRTA  
CC nucleic acids and proteins, and antibodies directed to an epitope of an  
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy  
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule  
CC that specifically hybridises with a unique sequence of human IRTA1-5; and  
CC treating a subject having a B cell cancer by administering an anti-IRTA  
CC antibody or an antisense oligonucleotide that specifically hybridises to  
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to  
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.  
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,  
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse  
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is  
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-  
CC Hodgkin's lymphoma  
XX  
XX

SQ Sequence 592 AA;

Query Match 74.2%; Score 2962; DB 4; Length 592;  
Best Local Similarity 98.6%; Pred. No. 8.3e-182;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60  
QY 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEQDSV 120  
DB 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEQDSV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVEPFTPLVRASSFPQISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
DB 181 VKIQVEPFTPLVRASSFPQISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240  
QY 241 LSPNQITAMWSKDSGFYWCACKAATPHSVISDSFRSMIQVQIPASHPVLTLSPKALNFE 300  
DB 241 LSPNQITAMWSKDSGFYWCACKAATPHSVISDSFRSMIQVQIPASHPVLTLSPKALNFE 300  
QY 301 GTKVTLHCETQEDSLRTLYRFHVEGVPLRHKSVCERGASISFSLTTENSNNYCTADNG 360  
DB 301 GTKVTLHCETQEDSLRTLYRFHVEGVPLRHKSVCERGASISFSLTTENSNNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNNYCTADNGFGPQRKAVSLSIITVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNNYCTADNGFGPQRKAVSLSIITVSHPVLTLSA 480  
QY 481 EALTTEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPVGVSFSLTEGHSGNYY 540  
DB 481 EALTTEGATVTLHCEVQRGSPQILYQFVHEDMPLWSSSTPVGVSFSLTEGHSGNYY 540

QY 541 CTADNGFGPQRSEVSVLSFVT-----VPVSRPIL 568  
DB 541 CTADNGFGPQRSEVSVLSFVTGKCVLASHPPL 572

RESULT 9

ADM35236

ID ADM35236 standard; protein; 592 AA.

XX ADM35236;

XX 03-JUN-2004 (first entry)

XX Human LY1448P cancer related protein for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;

XX chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

XX 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample

PT from the patient with a binding agent that binds to a cancer-associated

PT polypeptide and comparing the amount of polypeptide to a predetermined

PT cutoff value.

XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient

CC by: (i) contacting a biological sample from the patient with an agent

CC that binds to any of three polypeptides given in the specification; (ii)

CC detecting in a sample an amount of the peptide that binds to the binding

CC agent; and (iii) comparing the amount of polypeptide present in the

CC patient's sample to a predetermined cutoff value. The specification also

CC discloses a separate method for detecting (M2) cancer in a patient by a

CC method similar to M1, except that the detection agent is an

CC oligonucleotide that binds to any of three polynucleotides given in the

CC specification. M1 and M2 are useful for detecting the presence of cancer

CC in a patient, especially chronic lymphocytic leukemia. The applicants

CC have identified specific human polypeptides overexpressed in one or more

CC types of hematological malignancies. This sequence corresponds to a

CC protein used in the method of the invention.

XX Sequence 592 AA;

Query Match 74.2%; Score 2962; DB 7; Length 592;

Best Local Similarity 98.6%; Pred. No. 8.3e-182;

Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60

DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60

QY 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEQDSV 120

DB 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILQAPLSVFEQDSV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180

DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180



Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLVKONGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQBPFPTRPVLASSFQIPISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQDTLGLGWS 240  
Db 181 VKIQVQBPFPTRPVLASSFQIPISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQDTLGLGWS 240  
Qy 241 LSPNFQITAMKSKDSGFYCKAATMPHSVTSIDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Db 241 LSPNFQITAMKSKDSGFYCKAATMPHSVTSIDSPRSWIQVQIPASHPVLTLSPEKALNFE 300  
Qy 301 GTKVTLTCEQEDSLRTLRYFYHGVPLRHKSVCERGASISFSLTTEGNSGNYCTADNG 360  
Db 301 GTKVTLTCEQEDSLRTLRYFYHGVPLRHKSVCERGASISFSLTTEGNSGNYCTADNG 360  
Qy 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420  
Db 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420  
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVTPVSHPVLTLSA 480  
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVTPVSHPVLTLSA 480  
Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSITTECHSGNYY 540  
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSITTECHSGNYY 540  
Qy 541 CTADNGFGPQSRSEVSLFVT----VPVSRPIL 568  
Db 541 CTADNGFGPQSRSEVSLFVTCKWVLASHPPL 572  
RESULT 10  
ID ABU99155 standard; protein; 582 AA.  
XX AC ABU99155;  
XX DT 01-AUG-2003 (first entry)  
XX DE Novel human GPCR related protein NOV17a.  
XX KW Human; G-protein coupled receptor related protein; GPCR related protein;  
KW NOV; cytosolic; cardiant; antiarteriosclerotic; antidiabetic;  
KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;  
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;  
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;  
KW diabetes; immune disorder; AIDS; obesity; asthma;  
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
KW infection; multiple sclerosis; cancer-associated cachexia;  
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;  
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;  
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.  
XX OS Homo sapiens.  
XX WO200299116-A2.  
XX PD 12-DEC-2002.  
XX PF 04-JUN-2001; 2002WO-US017428.  
XX PR 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 15-JUN-2001; 2001US-0298556P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 28-JUN-2001; 2001US-0301550P.  
PR 13-AUG-2001; 2001US-0311972P.  
PR 27-AUG-2001; 2001US-0315071P.  
PR 29-AUG-2001; 2001US-0315660P.

PR 14-SEP-2001; 2001US-0322993P.  
PR 17-SEP-2001; 2001US-0322706P.  
PR 14-DEC-2001; 2001US-0341186P.  
PR 28-FEB-2002; 2002US-0361189P.  
PR 12-MAR-2002; 2002US-0363673P.  
PR 12-MAR-2002; 2002US-0363676P.  
PR 03-JUN-2002; 2002US-00363676.  
XX (CURA-) CURAGEN CORP.  
XX PA  
PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR,  
PI Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L,  
PI Macdougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; CAM;  
PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet BD;  
PI Voss EZ, Zerhusen BD;  
XX WPI; 2003-140627/13.  
DR N-PSDB; AC003659.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX PS Claim 1; Page 166; 332pp; English.  
XX  
CC The invention describes an isolated polypeptide (I) comprising any of 27  
CC 118-961 residue amino acid sequences, given in the specification, a  
CC mature form of them, a sequence that is at least 95 % identical to them,  
CC or a sequence having one or more conservative substitutions in them. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease selected from a pathology  
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides  
CC and antibodies are useful in treating or preventing NOVX-associated  
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
CC associated cachexia, and other wasting disorders associated with chronic  
CC diseases. The nucleic acids and polypeptides may also be used as targets  
CC for the identification of small molecules that modulate or inhibit e.g.  
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
CC wound healing and angiogenesis, in gene therapy, in generation of  
CC antibodies that bind immunospecifically to NOVX substances for use in  
CC therapeutic or diagnostic methods. The nucleic acids are further used as  
CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
CC medicine, and pharmacogenomics. The polypeptides are also useful as  
CC vaccines. This is the amino acid sequence of a novel human G-protein  
CC coupled receptor related protein NOV  
XX Sequence 582 AA;  
Qy Query Match 35.5%; Score 1419.5; DB 6; Length 582;  
Best Local Similarity 41.7%; Pred. No. 1e-82;  
Matches 316; Conservative 72; Mismatches 175; Indels 195; Gaps 9;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIILQFPWTTVFGERVLTACKGFRFYSQ-KTKWYH 59  
Db 1 MLLWVILLVLPVSGQFARTPRPIILQFPWTTVFGERVLTACKGFRFYSQ-KTKWYH 60  
Qy 60 RYLGKILRETPDNILEVOESGYRCAQGSPLSSPVHLDFSSASLILQPLSVFEGDSV 119  
Db 61 ---DEKLLIKHKDKI-QITEPGNYQCKTRGSSLSDAHVFEFSDWLLILQALHPVFEQDNV 116  
Qy 120 VLRCAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLVKONGAYRCTGYKESCC 176  
Db 117 LIRCQKDNKNTKQKYYKDGKOLPNSYLEKTVNSVRDMSKYHCTATRKFYLDIEV 176  
Qy 177 SSNTVQIQOEPTTRPVLASSFQIPISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQDTLG 236  
Db 177 TSKPLNIQVQELFHPVLRASSSTPIEGSPMTLTCTETQLSPQPDVQLQSLFRDSTQLG 236  
Qy 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVTSIDSPRSWIQVQIPASHPVLTLSPEKA 296  
Db 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVTSIDSPRSWIQVQIPASHPVLTLSPEKA 296

Db 237 LWSRSPRLQIPAMWTDGSGYWCVEVTWTHSIKRSLSRQIRVQ----- 281  
Qy 297 LNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASTSFSLTITNSGNYCT 356  
Db 282 ----- 281  
Qy 357 ADNGLGAKPSKAVSLVTVFVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHH 416  
Db 282 -----RVPSNVNLEIRPTGGQLIEGENMVLICSAVQSGGTFTFSMHK 324  
Qy 417 ED--AALERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLGITVPSHPV 474  
Db 325 EGRVSLGRKT-----QRLLAELH-----V 345  
Qy 475 LTLSSAEALTFEATVTLHCEVQSGPQILYQFYHEDMPLNMSSTPVSGRVFSFSLTEG 534  
Db 346 LIVKESDA----- 353  
Qy 535 HSGNYCTADNGFGPORSVSLFVTVFVSRPILTLRVPRQAQVVDLLELHCEAPRGSP 594  
Db 354 --GRYYCAADNVHSPILSTWIRVTRIPVSHFVLTFRAPRAHTVVDLLELHCEBSLRGSP 411  
Qy 595 PILYFVYHEDVTLGSSSAPSGEASPNLSLTAHSGNYSCEANNGLVAQHSPTISLSIV 654  
Db 412 PILYFVYHEDVTLGNSAASGASPNLSLTAHSGNYSCEADNGLGAQSHGVSRLVTV 471  
Qy 655 PVSRLPILTPRAQAQVVDLLELHCEALRGSPILYFVYHEDVTLGKISAPSGGGASFN 714  
Db 472 PVSRLPILTPRAQAQVVDLLELHCEALRGSPILYFVYHEDVTLGKISAPSGGGASFN 531  
Qy 715 LSLTTHSGIYSCADNGLEAQRSEMVTLKAVGEWALP 752  
Db 532 LSLTTHSGIYSCADNGLEAQRSEMVTLKAVGEWALP 569  
RESULT 11  
ADN93875  
ID ADM93875 standard; protein; 582 AA.  
AC ADM93875;  
DT 17-JUN-2004 (first entry)  
XX Human NOV protein #47.  
DE gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;  
KW Parkinson's disease; metabolic disorder; diabetes; obesity;  
KW immune related disorder; tissue typing; human.  
XX Homo sapiens.  
OS US2004009480-A1.  
XX 15-JAN-2004.  
XX 03-JUN-2002; 2002US-00162335.  
XX 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 11-JUN-2001; 2001US-0297414P.  
PR 12-JUN-2001; 2001US-0297567P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 15-JUN-2001; 2001US-0298556P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 28-JUN-2001; 2001US-0301500P.  
PR 13-AUG-2001; 2001US-0311972P.  
PR 27-AUG-2001; 2001US-0315071P.  
PR 29-AUG-2001; 2001US-0315660P.  
PR 14-SEP-2001; 2001US-0322293P.

PR 17-SEP-2001; 2001US-0322706P.  
PR 14-DEC-2001; 2001US-0341186P.  
PR 28-FEB-2002; 2002US-0361189P.  
PR 12-MAR-2002; 2002US-0363673P.  
PR 12-MAR-2002; 2002US-0363676P.  
XX  
PA (ANDE/) ANDERSON D W.  
PA (BAUM/) BAUMGARTNER J C.  
PA (BOLD/) BOLD OG F L.  
PA (CASM/) CASHMAN S J.  
PA (EDIN/) EDINGER S R.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUOX/) GUO X S.  
PA (HUAL/) HJALT T.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
PA (STON/) STONE D J.  
PA (SPYT/) SPYTEK K A.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
XX  
PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR, Li L;  
PI Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjal T, Kekuda R, Li L;  
PI MacDougall JR, Malyankar UM, Millet I, Padigar M, Patturajan M;  
PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CM;  
PI Voss EZ, Zerhusen BD;  
XX WPI: 2004-090456/09.  
DR N-PSDB; ADM93874.  
XX  
PT New NOVX polypeptide, useful for preparing a composition for treating or  
PT preventing e.g., cancer, neurodegenerative disorders such as Parkinson's  
PT disease, or metabolic disorders such as diabetes or obesity, or for  
PT tissue typing.  
XX  
PS Claim 1; SEQ ID NO 94; 202pp; English.  
XX  
CC The invention relates to an isolated NOVX polypeptide. The polypeptide is  
CC useful for preparing a composition for treating or preventing a pathology  
CC associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders  
CC such as Parkinson's disease, metabolic disorders such as diabetes or  
CC obesity or immune related disorders or for tissue typing. The present  
CC sequence represents a human NOV protein.  
XX  
SQ Sequence 582 AA;  
Query Match 35.5%; Score 1419.5; DB 8; Length 582;  
Best Local Similarity 41.7%; Pred. No. 1e-82;  
Matches 316; Conservative 72; Mismatches 175; Indels 195; Gaps 9;  
Qy 1 MLILWILLVLAIPVSGQFARTPRPIIFLOPPVTTVFGGERVTLTKGFRFYSQ-KTKWYH 59  
Db 1 MLILWILLVLTGREGSGVAPKAVILLNPPWSTAFKGVKVALICSSISLSLAQGTYYWH 60  
Qy 60 RYLKKEILRETDPNILEVOESGEYRCQAQSGPLSSPVLHDFSSASLILQAPLVSFEGDSV 119  
Db 61 ----DEKLLIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116  
Qy 120 VLFCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHIFACLKDKNGAYRCTGKESC---CPV 176  
Db 117 ILRCQCKDNKNTKQVYKDGKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFIYLDIEV 176

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QY 177 SNTVKIQVQEPTRPVRVLRASSPQISGNPVTLTCETQLSLERSDVPRLRFRFRDDDTLG 236
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTLTCTQLSPDRDVLQQLSFRDSOTLG 236
QY 237 LGWSLSNFOITAMWSKDSGYMCKAATMPHSVSDSPRSWIOVQIPASHVLTLSPEKA 296
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
237 LGWSRSPRLQIPAMWTEDSSGYCEVETVTHSIKRSLSRQIRVQ----- 281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGYYCT 356
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
282 ----- 281
QY 357 ADNGLGAKPSKAVSLSVTVPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGLPILYQFHH 416
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
282 -----RVPSNVNLEIRPTGGQIEGENNVILCSVAQSGSTVTFSSWHK 324
QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPV 474
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 EGRVRSIGRKT-----QSLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 535 HSGNYYCTADNGFGPQRSEVSVLFTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSP 594
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
354 --GRYYCAADNVHSPILSTWIRVTRIPVSHPLVTFRAPRAHTVVGDLLELHCESLRGSP 411
QY 595 PILYFYHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTLSLVIV 654
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
412 PILYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCEADNGLGAQHSGLVSRVTV 471
QY 655 PVSRLPILTFRAPRAQAVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFN 714
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472 PVSRLPILTRAPGAQAVVGDLLELHCESLRGSPILYFYHEDVTLGKISAPSGGASFN 531
QY 715 LSLTTEHSGIYSCADNGLRAQRSEMTLKVAGSWALP 752
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
532 LSLTTEHSGNYSCEADNGLGAQHSKVTLNVTGLVLP 569

RESULT 12
ID ADM06089
XX ADM06089 standard; protein; 707 AA.
AC ADM06089;
XX
XX
XX 20-MAY-2004 (first entry)
DT
XX Human protein of the invention SEQ ID NO:4774.
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX
XX EP1347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI: 2003-723558/69.
XX N-PSDB; ADM03646.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
```

```
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX Claim 1; SEQ ID NO 4774; 305pp; English.
PS
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
XX protein sequence of the invention.
SQ Sequence 707 AA;

Query Match 35.5%; Score 1417.5; DB 7; Length 707;
Best Local Similarity 41.6%; Pred. No. 1.8e-82;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

QY 1 MLLWVILLVLPVSGOPARTPRPIIFLOPPMTTVFOGERVTLCKGFRFYSPQ-KTKWYH 59
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MLLWVILLVLPVSGOPARTPRPIIFLOPPMTTVFOGERVTLCKGFRFYSPQ-KTKWYH 60
QY 60 RYLKGEILRETPDNILEVQESGEYRQAOQSPSSPVHLDFSSASLILQAPLSVFEGDSV 119
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVEGDNV 116
QY 120 VLRCAKAEVTLNNTYIKNDNVLAFLNKRDFHIFHACLKNDGAYRCTGYKESC---CPV 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
117 ILRCQCKNDKNTKQVYKDGKQLPNSYNLEKIVTNSVSRDNSKYCHTAYRKFYLDIEV 176
QY 177 SNTVKIQVQEPTRPVRVLRASSPQISGNPVTLTCETQLSLERSDVPRLRFRFRDDDTLG 236
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTLTCTQLSPDRDVLQQLSFRDSOTLG 236
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237 LGWSRSPRLQIPAMWTEDSSGYCEVETVTHSIKRSLSRQIRVQ----- 281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGYYCT 356
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QY 357 ADNGLGAKPSKAVSLSVTVPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGLPILYQFHH 416
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282 -----RVPSNVNLEIRPTGGQIEGENNVILCSVAQSGSTVTFSSWHK 324
QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPV 474
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 EGRVRSIGRKT-----QSLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
346 LTVKESDA----- 353
QY 535 HSGNYYCTADNGFGPQRSEVSVLFTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSP 594
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354 --GRYYCAADNVHSPILSTWIRVTRIPVSHPLVTFRAPRAHTVVGDLLELHCESLRGSP 411
QY 595 PILYFYHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTLSLVIV 654
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412 PILYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCEADNGLGAQHSGLVSRVTV 471
QY 655 PVSRLPILTFRAPRAQAVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFN 714
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472 PVSRLPILTRAPGAQAVVGDLLELHCESLRGSPILYFYHEDVTLGKISAPSGGASFN 531
QY 715 LSLTTEHSGIYSCADNGLRAQRSEMTLKVAGSWALP 759
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
532 LSLTTEHSGNYSCEADNGLGAQHSKVTLNVTGLNVTG-----TSRN 568
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CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX	SQ Sequence 750 AA;									
Query Match		35.5%; Score 1417.5; DB 8; Length 750;								
Best Local Similarity		41.6%; Pred. No. 1.9e-82;								
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;										
QY	1	MLLWVLLVAVSGOFARTPRPIIFLOPPPTTVFQGERVTLTKGFRFYSPQ-KTKWYH	59							
DB	1	MLLWVLLVAVSGOFARTPRPIIFLOPPPTTVFQGERVTLTKGFRFYSPQ-KTKWYH	60							
QY	60	RYLKGRIILRETPTDNIIEVOESGEYRCQAGSPFLSPVHLDFSSASLILOAPLSVFEQDSV	119							
DB	61	---DEKLLAKIKDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVEGDV	116							
QY	120	VLCRAKAEVTLNNTIYKNDVLAFLNKTDPHIACLKONGAYRCTYKESC---CPV	176							
DB	117	ILRCQKDNKNTKQKYYKDGKQLPNSYNLEKITVNSVRDNDKYHCTAYRKFYILDIEV	176							
QY	177	SSNTVKIOVEPTREPVLRASSFOPTISGNPVTILCTETOLSLERSDVPLRFRFRDDQTLG	236							
DB	177	TSKPLNIQVQELFLHVLRLASSSTPIEGSPMTLCTETQLSPQRPDVLQFSLFRDSQTLG	236							
QY	237	LGMSLSPNFQITAMWSKDSGFYCKAATMPHVSVIDSPRSWIQVQIPASHPVLTLSPEKA	296							
DB	237	LGMSPRLQIPAMWTEDSGYVCEVETVTHSKKRLSRQIRVQ-----	281							
QY	297	LNFEGTIVLHCETQDSLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTENSGNYICT	356							
DB	282	-----	281							
QY	357	ADNGLGAKPSKAVSLSVTVPSHVPVNLSSPEDLIPEGAKVTILHCEAQSGSLPILYQFHH	416							
DB	282	-----RVPVSNVLEIRPTGGQLIEGENMVLICSVAGSGGTVTFSMHK	324							
QY	417	ED--NALERRANSAGGVAISFLTAHSGNYYCTADNGFGPQSKAVSLITVPVSHPV	474							
DB	325	EGRVRSIGRKT-----QRSLLAEHL-----V	345							
QY	475	LTLLSSAEALTPEGATVILHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSGFSLSLREG	534							
DB	346	LTAKESDA-----	353							
QY	535	HSGNYYCTADNGFGPQSKAVSLSVTVPSHVPVNLSSPEDLIPEGAKVTILHCEAQSGSLPILYQFHH	594							
DB	354	--GRYYCAADNVHSPILSTWIRVTRIPVSHVPVLTFRAPRAHTVVGDLLEHCESLRGSP	411							
QY	595	PILYWFYHEDVTLGSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVAQHSDTISLSVIV	654							
DB	412	PILYRFYHEDVTLGNSAPSGGSEASFNLSLTAHSGNYSCEANNGLVAQHSDTISLSVIV	714							
QY	655	PVSRPILTRAPRAQAVVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGSEASFN	714							
DB	472	PVSRPILTRAPRAQAVVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGSEASFN	531							
QY	715	LSLTTEHSGIYSCADNGLQAQSEMVTILKAGEWALPTSTSEN	759							
DB	532	LSLTTEHSGIYSCADNGLQAQSEMVTILKAGEWALPTSTSEN	568							

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Job time : 100.809 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:27:40 ; Search time 25.4304 Seconds  
(without alignments)  
2227.987 Million cell updates/sec

Title: US-09-724-254A-44  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3792.5	95.0	1248	4	US-09-949-016-10595 Sequence 10595, A
2	3792.5	95.0	1248	4	US-09-949-016-10596 Sequence 10596, A
3	386	9.7	261	4	US-09-245-764-7 Sequence 7, Appl
4	369.5	9.3	4391	4	US-10-006-011A-2 Sequence 2, Appl
5	317.5	8.0	1709	4	US-09-949-016-10503 Sequence 10503, A
6	305.5	7.7	254	2	US-08-667-939A-3 Sequence 3, Appl
7	305.5	7.7	254	2	US-08-433-123-3 Sequence 3, Appl
8	304.5	7.6	254	2	US-08-667-939A-2 Sequence 2, Appl
9	304.5	7.6	254	4	US-08-433-123-2 Sequence 2, Appl
10	296.5	7.4	738	3	US-08-478-208-32 Sequence 32, Appl
11	296.5	7.4	738	4	US-09-336-536-73 Sequence 73, Appl
12	293	7.3	233	2	US-08-667-939A-6 Sequence 6, Appl
13	293	7.3	233	4	US-08-433-123-6 Sequence 6, Appl
14	292.5	7.3	254	2	US-08-667-939A-9 Sequence 9, Appl
15	292.5	7.3	254	4	US-08-433-123-9 Sequence 9, Appl
16	292	7.3	233	2	US-08-667-939A-5 Sequence 5, Appl
17	292	7.3	233	2	US-08-667-939A-8 Sequence 8, Appl
18	292	7.3	233	4	US-08-433-123-5 Sequence 5, Appl
19	292	7.3	233	4	US-08-433-123-8 Sequence 8, Appl
20	290	7.3	315	4	US-09-949-016-11121 Sequence 11121, A
21	290	7.3	315	4	US-09-949-016-11122 Sequence 11122, A
22	288.5	7.2	254	2	US-08-667-939A-4 Sequence 4, Appl
23	288.5	7.2	254	4	US-08-433-123-4 Sequence 4, Appl
24	286	7.2	233	2	US-08-667-939A-7 Sequence 7, Appl
25	286	7.2	233	4	US-08-433-123-7 Sequence 7, Appl
26	285.5	7.2	254	2	US-08-667-939A-1 Sequence 1, Appl
27	285.5	7.2	254	4	US-08-433-123-1 Sequence 1, Appl

28	285.5	7.2	738	6	5264554-2	Patent No. 5264554
29	285.5	7.2	738	6	5264554-2	Patent No. 5264554
30	280.5	7.0	698	2	US-08-602-725-36	Sequence 36, Appl
31	280.5	7.0	702	4	US-09-949-016-6484	Sequence 6484, Ap
32	280.5	7.0	734	2	US-08-389-459A-17	Sequence 17, Appl
33	280.5	7.0	734	3	US-08-987-867A-17	Sequence 17, Appl
34	280.5	7.0	740	4	US-09-949-016-8168	Sequence 8168, Ap
35	275	6.9	197	3	US-08-788-954-2	Sequence 2, Appl
36	275	6.9	203	2	US-08-667-939A-20	Sequence 20, Appl
37	275	6.9	203	4	US-08-433-123-20	Sequence 20, Appl
38	274	6.9	174	4	US-09-245-764-8	Sequence 8, Appl
39	271	6.8	215	2	US-08-667-939A-18	Sequence 18, Appl
40	271	6.8	215	4	US-08-433-123-18	Sequence 18, Appl
41	269.5	6.7	199	2	US-08-768-964-12	Sequence 12, Appl
42	269.5	6.7	199	3	US-09-005-299-12	Sequence 12, Appl
43	269.5	6.7	199	3	US-09-515-431-12	Sequence 12, Appl
44	269.5	6.7	263	2	US-08-768-964-2	Sequence 2, Appl
45	269.5	6.7	263	3	US-09-005-299-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10595  
; Sequence 10595, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10595  
; LENGTH: 1248  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10595

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Best Local Similarity	97.1%	Pred. No.	0				
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Gaps	2						
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Db	476	MLLWVILLVLPVSGQFARTPRIIIFLOPWTTFVQGERVTLTKGFRFYSPOKTKYHR	535				
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSGPLSPVHLDFSSASLILOAPLSPEGDSVV	120				
Db	536	YLKKEILRETPDNILEVQESGEYRCQAQSGPLSPVHLDFSSASLILOAPLSPEGDSVV	595				
QY	121	LRCRAAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT	180				
Db	596	LRCRAAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKDNGAYRCTGYKESCCPVSSNT	655				
QY	181	VKIQVEPFRPVLRASSQFISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS	240				
Db	656	VKIQVEPFRPVLRASSQFISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS	715				
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHVPLVTLSPKALNFE	300				
Db	716	LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHVPLVTLSPKALNFE	775				
QY	301	GTKVTLHCQEDSLRTLRYFYHEGVPLRHKSVRCRGASISFSLTTENSNGNYCTADNG	360				

Db 776 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 835  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 836 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 895  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTPVSHPVNLSS 480  
Db 896 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTPVSHPVNLSS 955  
Qy 481 EALTFCATVTLHCEVQSGPQILYQFHYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 540  
Db 956 EALTFCATVTLHCEVQSGPQILYQFHYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 1015  
Qy 541 CTADNGFGPQSEVSVLFTVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600  
Db 1016 CTADNGFGPQSEVSVLFTVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 1073  
Qy 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660  
Db 1074 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 1133  
Qy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYQFHYHEDVTLGKISAPSGGASFNLSLITE 720  
Db 1134 LTRAPRAQAVVGDLLEHCEALRGSSPILYQFHYHEDVTLGKISAPSGGASFNLSLITE 1174  
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVAGE 748  
Db 1175 HSGIYSCDADNGLEAQRSEMVTLKVAGE 1202  
RESULT 2  
US-09-949-016-10596  
; Sequence 10596 Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10596  
; LENGTH: 1248  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10596  
Query Match 95.0%; Score 3792.5; DB 4; Length 1248;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 726; Conservative 0; Mismatches 1; Indels 21; Gaps 2;  
Qy 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60  
Db 476 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 535  
Qy 61 YLGKILRETPDNILEVESEGYRQACQSPVSLDFSSASLILOAPLSVPEGDSVV 120  
Db 536 YLGKILRETPDNILEVESEGYRQACQSPVSLDFSSASLILOAPLSVPEGDSVV 595  
Qy 121 LRCRAKAEVTLNNTYKNDVLAFLNKRDTDPHIACILKNGAVRCTGKESCCPVSNT 180  
Db 596 LRCRAKAEVTLNNTYKNDVLAFLNKRDTDPHIACILKNGAVRCTGKESCCPVSNT 655

Qy 181 VKIQVCEPPTRPVLRASSFPQISGNPVTILTCETQSLERSDVPLRFRFRDDQDTLGLGWS 240  
Db 656 VKIQVCEPPTRPVLRASSFPQISGNPVTILTCETQSLERSDVPLRFRFRDDQDTLGLGWS 715  
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300  
Db 716 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 775  
Qy 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360  
Db 776 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 835  
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
Db 836 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 895  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTPVSHPVNLSS 480  
Db 896 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTPVSHPVNLSS 955  
Qy 481 EALTFCATVTLHCEVQSGPQILYQFHYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 540  
Db 956 EALTFCATVTLHCEVQSGPQILYQFHYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 1015  
Qy 541 CTADNGFGPQSEVSVLFTVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600  
Db 1016 CTADNGFGPQSEVSVLFTVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 1073  
Qy 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660  
Db 1074 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 1133  
Qy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYQFHYHEDVTLGKISAPSGGASFNLSLITE 720  
Db 1134 LTRAPRAQAVVGDLLEHCEALRGSSPILYQFHYHEDVTLGKISAPSGGASFNLSLITE 1174  
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVAGE 748  
Db 1175 HSGIYSCDADNGLEAQRSEMVTLKVAGE 1202  
RESULT 3  
US-09-245-764-7  
; Sequence 7, Application US/09245764  
; Patent No. 6675105  
; GENERAL INFORMATION:  
; APPLICANT: Hogarth, P. Mark  
; APPLICANT: Powell, Maree S.  
; APPLICANT: McKenzie, Ian F.C.  
; APPLICANT: Maxwell, Kelly F.  
; APPLICANT: Garrett, Thomas P.J.  
; APPLICANT: Epa, Vidana  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 4102-4  
; CURRENT APPLICATION NUMBER: US/09/245,764  
; EARLIER FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: 60/099,994  
; EARLIER FILING DATE: 1998-09-11  
; EARLIER APPLICATION NUMBER: 60/073,972  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-245-764-7  
Query Match 9.7%; Score 386; DB 4; Length 261;  
Best Local Similarity 35.7%; Pred. No. 3 8e-26;  
Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;





QY	233	QTLGLGWSLSPN---FQITAMWKSODGGPYCKCAATPHSHVSDSPRSWIOVQIPASHPVL	289
Db	461	HSRPSGTSGPNSLRLEIRDLLEETDSGYKCSATNSLGNATS-----TUDFFHANAARL	513
QY	290	TLSPEKALNFECTVTLHCET---QEDSLRPLY---RFYHIEGVPLRHKSVRCERGASIS	342
Db	514	LISPAAEV-VEGOAVTLSCRGLSTPDPARFSWYINGALLHEG-----PGSSILL	561
QY	343	F-SLATTENSGNYCTADNGLGAK-PSKAVSLSVTVPVSHPVNLSSPEDLIFEGAKVTLH	400
Db	562	LPAASSTDAGSYHCRARDGHSASGSSPAVLTVLPPROPTTTTRLDLDAAGAGA-----	616
QY	401	CBAQRGSL-----PILYQFHEDAALERR-----SANSAGGVAISPSLT-----	439
Db	617	---GRRGLLCRVDSDDPARLOLLHKDRVVATSLPSGGGCSCTGGCSPRMKVTKAPNLLRV	674
QY	440	-----AEHSGNYCTADNGFGFQORSKAVSLSTTVPVSHPVLTLSAAELTFEGAVTLH	493
Db	675	EIHNPILLEEGLYLCEASNAIG-----NASTSATFNGQATVLAIPASHTLQ-EGTEANLT	728
QY	494	CEYQR-----GSPQ	502
Db	729	CNVSREAAAGSPANFNSFRNGVILWAQGPLETVTLTPVARTDAALYACRILTEAQAULSTPV	788
QY	503	ILYQFTHEDMPLWSS-----STPSVG	523
Db	789	LLSVLYPPDRPKLSALLDMCGHMAIFICTVDSRPLALLALFGEHLLATSLGQVPVSHG	848
QY	524	RV-----SFSFSLTE---GHSNGNYCTADNGFGFQORSEVSLFVTVPVSRPILTLRVP	573
Db	849	RFQAKAEANSLKLEVRLELGLDSSGYRCEATNVLG---SSNTSLIFFQV---RGAWVQVSP	902
QY	574	RAQAVWGDLLELHCEAPRGSP-ILYWFYHEDVTLGSSSAPSGEASFNLSLTAEHSGNY	632
Db	903	SPELQEGQAVVLSQCVPTGVPPEGTSYRWYRDGQFOESTSATLRF-----AITLTQAGAY	958
QY	633	SCEANNGVLAQHSPTISIVTVPVSRPILTFRAPQAQV-----GDILLELHCEALRG	685
Db	959	HCQARQ---APGSATTSUA---VPIS---LHVSYAPRHVTLTLMDTGPRGLGLLLCR-VDS	1009
QY	686	SSPILYWFYHED---VTLGKISAPSGGGASFNLSLT-----TEHSGIYSCEA	729
Db	1010	DPQAQLRLHGLDRIVASTLOQGVGPEGSSPRLHVAVAPNTLRLRIHGAMLEDEGVYICEA	1069
QY	730	DNGL	733
Db	1070	SNTL	1073

RESULT 6  
US-08-667-939A-3  
; Sequence 3, Application US/08667939A  
; Patent No. 5998166  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,939A  
; FILING DATE: 24-JUN-1996  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/433,123  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LUO-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-667-939A-3

Query Match 7.7%; Score 305.5; DB 2; Length 254;  
Best Local Similarity 32.9%; Pred. No. 5.6e-19;  
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY 1 MLLWVILLVLAPVSGOFARTPIIFLOPPWTTVFGQSERVLTCKGFFRYGQ--KTKWY 58  
Db 4 LLLPTALLLVSGMRTEDLPRAVVFLEQWVRVLEKDSVTLKCGQ--AYSPEDNSTQWF 61  
QY 59 HRYLGKIEILRETPDNILE-----VOESGEYRCQAGSPLLSPVHLDFSSASLI 106  
Db 62 HK-----ENLISQASSYFIDAATVDSGEYRCQTNLSDPVQLEVQVGWLL 110  
QY 107 LQAPLSVP-EGDSVULRCRAKAEVTILNNTIY-KNDVLAFALNKRITDFIHPACLKNGAY 164  
Db 111 LQAPRWYFKGEDPIHLRCHGSKWNTALHKVTYLONGKDKRYFHNSDFHPRATLKDSGY 170  
QY 165 RCTGKESCCPVSNNTVKIQVQEPFTRPVLRASSFPQISGNPVTTCTCTQLSLERSDPL 224  
Db 171 FCRGLVGS-KNVSEVTNITITGLA--VSTISSPP-PGYQVSF-CLVMVLLFAVDT-- 223  
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 -----GLYFSVKTNIIRSTRDWKHKFKWRK 249

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RESULT 7
US-08-433-123-3
; Sequence 3, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

```

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; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-3

Query Match
Best Local Similarity 32.9%; Pred. No. 5.6e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEDLPKAVFLEPQWRYVLEKDSVTLKCG--AYSPEINSTQWF 61
QY 59 HRYLKGKILRETPDNILE-----VQSGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVQVGVWLL 110
QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHDFHIFHACIKONGAY 164
Db 111 LQAPRWVFKEDPIHLRCHSKWNTALHKVTYLONGKDKRKYFHNSDFHIFKATLKDSGSY 170
QY 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRRASSFQISGNPVTLTCTETOLSLSERSDVPL 224
Db 171 FCRLGVCS-KNVSETVNIITQGLA--VSTISSFFP-PGYQVSF-CLVWVLLFAVDV-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 -----GLYFSVKTNRSTRDWDKHKFKWK 249

RESULT 8
US-08-667-939A-2
; Sequence 2, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-2

Query Match
Best Local Similarity 32.9%; Pred. No. 6.8e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEDLPKAVFLEPQWRYVLEKDSVTLKCG--AYSPEINSTQWF 61
QY 59 HRYLKGKILRETPDNILE-----VQSGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVQVGVWLL 110
QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHDFHIFHACIKONGAY 164
Db 111 LQAPRWVFKEDPIHLRCHSKWNTALHKVTYLONGKDKRKYFHNSDFHIFKATLKDSGSY 170
QY 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRRASSFQISGNPVTLTCTETOLSLSERSDVPL 224
Db 171 FCRLGVCS-KNVSETVNIITQGLA--VSTISSFFP-PGYQVSF-CLVWVLLFAVDV-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 -----GLYFSVKTNRSTRDWDKHKFKWK 249

RESULT 9
US-08-433-123-2
; Sequence 2, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-2

Query Match
Best Local Similarity 32.9%; Pred. No. 6.8e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;

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Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;  
QY 1 MLLWVILVAVSQPARTPPIFIOPPTTVOGERVTLCTCKGRFFYSQ--KTKWY 58  
Db 4 LLLPTALLLLSAGWRTDELKPAVVFLEPQWYVLEKSDSVTLKCG--AYSPDNSTQWP 61  
QY 59 HRYLKGELILRETPDNILE-----VOESGEYRCQAQGGSPPLSPVHLDFSSASLI 106  
Db 62 HK-----ENLISQASSYFIDAATVDDSGEYRCQNLSTLSDPVQLEVQVGWLL 110  
QY 107 LOAPLSVF--EGDSVVLRCRAKAEVTLNNIY--KDNVLAFLNKRTDFH PHACLKONGAY 164  
Db 111 LQAPRVFKEEDPIHLRCHSWKNTALHKVTVLQNGKDRKYFHNSDPHIPKATLKDSGY 170  
QY 165 RCTGYKESCCPVSSNTVKIQVEPTFRPVLRASSFPQISGNPVTLTCTQLSLERSDVL 224  
Db 171 FCKGLVGS--KNYSSETVNITIIQGLA--VSTNSFFP--PGQVSP--CLVMVLLFAVDI-- 223  
QY 225 RFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWK 261  
Db 224 -----GLYFSKTNIRSTRDKDKHFKWRK 249

RESULT 10  
US-08-478-208-32  
; Sequence 32, Application US/08478208A  
; Patent No. 6087331  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Peter J.  
; APPLICANT: Kumina, Richard J.  
; APPLICANT: Kirschbaum, Nancy  
; TITLE OF INVENTION: THERAPEUTIC USE OF PLATELET-ENDOTHELIAL CELL ADHESION  
; TITLE OF INVENTION: MOLECULE-1 COMPOSITIONS  
; FILE REFERENCE: 160180.90147  
; CURRENT APPLICATION NUMBER: US/08/478,208A  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 738  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-478-208-32

Query Match 7.4%; Score 296.5; DB 3; Length 738;  
Best Local Similarity 22.9%; Pred. No. 1.9e-17;  
Matches 136; Conservative 107; Mismatches 251; Indels 101; Gaps 26;  
QY 203 SGNPVTLCETQLSLERSDVL-RFRFRDDOTLGLGWSLSPNFQITAMWSK----- 253  
Db 49 NGKMLTLOCFADVSTTSHVRFQHQMLFYKDDVLF-----YNISMSKTESYFIPEV 99  
QY 254 ---DSGFYWCKAATMPHSVISDSRSPWIOVQ-----IPASHPVLTLSPKALNPEGTQVT 305  
Db 100 RIYDSGYKCTV-----IVNKEKTTAEYQLLVGVGPS--PRVTLDKKEAI--OGGIVR 149  
QY 306 LHCETQEDSLRTLRYFYHEGVPLRHKSVCERGAS-----ISFSLTTEN----- 349  
Db 150 VNCSPVEE--KAPIHFTIEKLELNKMWKLKREKSRDQNFVLEFFVEQDRVLSFRQ 207  
QY 350 ----SGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQR 405  
Db 208 ARIISGIIHQMTSES-----TKSELVTVESFSTPKFHI--SPTGMIMEGAQLHIKCTIQV 260  
QY 406 GSL-----PILYQFHEDDAL--ERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQR 458  
Db 261 THLAQEFPEIILIQ--KDKAIVAHNRHGNKA---VYSVMVMEHSGNTCKVES--RI 311  
QY 459 SKAVLSLITVPVSHVPLNLSSAEALTTFEGATVTLHCEVQGRSPQILYOFYHEDMPLWSSS 518  
Db 312 SKVSSIVNITELFSKPELESSFTHLDQGERLNLSCTIP--GAPPANFTIQEDTIV--SQ 368  
QY 519 TPSVGRVVSFSLTEGHSNGNYCYCTADNGFGPQRSEVSLFVTVPSRPILTLRVPRQAV 578  
Db 406 GSL-----PILYQFHEDDAL--ERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQR 458  
Db 261 THLAQEFPEIILIQ--KDKAIVAHNRHGNKA---VYSVMVMEHSGNTCKVES--RI 311  
QY 459 SKAVLSLITVPVSHVPLNLSSAEALTTFEGATVTLHCEVQGRSPQILYOFYHEDMPLWSSS 518  
Db 312 SKVSSIVNITELFSKPELESSFTHLDQGERLNLSCTIP--GAPPANFTIQEDTIV--SQ 368  
QY 519 TPSVGRVVSFSLTEGHSNGNYCYCTADNGFGPQRSEVSLFVTVPSRPILTLRVPRQAV 578

Db 369 TDQFTKIA-----SKSDSGTYICTAGIDKVKKSNVTQIVVCEMLSQPRISYDA-QFEVI 422  
QY 579 VGDLLHCEAPRGSPPILYFYHEDVTLTGSSASPGGEASFNLSLTAEHSGNYSCEANN 638  
Db 423 KGQTIIEVRCEISGTLPISYQLLKTISKVLENSTKNSNDPAVFKDNPTD--VEYQCVADN 480  
QY 639 --GLVAQHSDTISLVIVVSPILTFRAPRAQAVVGDLLHCEALRGSSPILYFYFHE 696  
Db 481 CHSHAKMLSEVLKRVIAPVDEVOISILSKV--VESGEDIVLOCAVNEGSGPITYKFYE 539  
QY 697 DVTGLKISAPSGGAGSF--NLSLTTEHSGIYSC---EADNGLEAQRSEKMTLKV 745  
Db 540 KEGKPFQMTSNATQAFWTKQKAKSEGEYCYTAFNRANHASSVPSRKILTVRV 594

RESULT 11  
US-09-336-536-73  
; Sequence 73, Application US/09336536  
; Patent No. 6406884  
; GENERAL INFORMATION:  
; APPLICANT: Leiby, K.  
; APPLICANT: McKay, C.  
; APPLICANT: Bossone, S.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-144  
; CURRENT APPLICATION NUMBER: US/09/336,536  
; CURRENT FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 738  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-336-536-73

Query Match 7.4%; Score 296.5; DB 4; Length 738;  
Best Local Similarity 22.9%; Pred. No. 1.9e-17;  
Matches 136; Conservative 107; Mismatches 251; Indels 101; Gaps 26;  
QY 203 SGNPVTLCETQLSLERSDVL-RFRFRDDOTLGLGWSLSPNFQITAMWSK----- 253  
Db 49 NGKMLTLOCFADVSTTSHVRFQHQMLFYKDDVLF-----YNISMSKTESYFIPEV 99  
QY 254 ---DSGFYWCKAATMPHSVISDSRSPWIOVQ-----IPASHPVLTLSPKALNPEGTQVT 305  
Db 100 RIYDSGYKCTV-----IVNKEKTTAEYQLLVGVGPS--PRVTLDKKEAI--OGGIVR 149  
QY 306 LHCETQEDSLRTLRYFYHEGVPLRHKSVCERGAS-----ISFSLTTEN----- 349  
Db 150 VNCSPVEE--KAPIHFTIEKLELNKMWKLKREKSRDQNFVLEFFVEQDRVLSFRQ 207  
QY 350 ----SGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQR 405  
Db 208 ARIISGIIHQMTSES-----TKSELVTVESFSTPKFHI--SPTGMIMEGAQLHIKCTIQV 260  
QY 406 GSL-----PILYQFHEDDAL--ERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQR 458  
Db 261 THLAQEFPEIILIQ--KDKAIVAHNRHGNKA---VYSVMVMEHSGNTCKVES--RI 311  
QY 459 SKAVLSLITVPVSHVPLNLSSAEALTTFEGATVTLHCEVQGRSPQILYOFYHEDMPLWSSS 518  
Db 312 SKVSSIVNITELFSKPELESSFTHLDQGERLNLSCTIP--GAPPANFTIQEDTIV--SQ 368  
QY 519 TPSVGRVVSFSLTEGHSNGNYCYCTADNGFGPQRSEVSLFVTVPSRPILTLRVPRQAV 578  
Db 369 TDQFTKIA-----SKSDSGTYICTAGIDKVKKSNVTQIVVCEMLSQPRISYDA-QFEVI 422  
QY 579 VGDLLHCEAPRGSPPILYFYHEDVTLTGSSASPGGEASFNLSLTAEHSGNYSCEANN 638  
Db 423 KGQTIIEVRCEISGTLPISYQLLKTISKVLENSTKNSNDPAVFKDNPTD--VEYQCVADN 480  
QY 639 --GLVAQHSDTISLVIVVSPILTFRAPRAQAVVGDLLHCEALRGSSPILYFYFHE 696

Db 481 CHSHAKMLSEVLRVKVIAPVDEVOISILSSKV-VESGEDIVLQCAVNEGSGPIYKIFYRE 539  
Qy 697 DVTILGKISAPSGGASF--NLSLTTEHSGIYSC----EADNGLAQRSEMVTLKV 745  
Db 540 KEGKPPQMTSNATQAFWTKQKASKEQEGEYCTAFNRRANHASSVPSPSKILTTRV 594

RESULT 12  
US-08-667-939A-6  
; Sequence 6, Application US/08667939A  
; Patent No. 5998166  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,939A  
; FILING DATE: 24-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/433,123  
; FILING DATE: 03-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-667-939A-6

Query Match 7.3%; Score 293; DB 2; Length 233;  
Best Local Similarity 34.7%; Pred. No. 6.3e-18;  
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

Qy 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPO--KTKWY 58  
Db 4 LLLPTALLLVLSAGMRTEPLKAVFLEPQWYRVLEKDSVTLKQCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQGSPLSSPVHLDFFSSASLI 106  
Db 62 HN-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110  
Qy 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPDHPHACILKONGAY 164  
Db 111 LQAPRWVFKEDPHLRCHSWKNTALHKVLYLQNGDKRKYFHNSDPHFKATLKDSGSY 170  
Qy 165 RCTGYKESCCPVSNVKIQVQEPFTRPVLRASSFPISGNPVTLCTETOLSERSDVPL 224  
Db 171 FCRGLVGS-KNVSSETVNITITQGLA--VSTISSFSF-PGVQVSF-CLVMVLLFAVDGTGL 225  
Qy 225 RF 226  
Db 226 YF 227

RESULT 14  
US-08-667-939A-9  
; Sequence 9, Application US/08667939A  
; Patent No. 5998166  
; GENERAL INFORMATION:

RESULT 13  
US-08-433-123-6  
; Sequence 6, Application US/08433123  
; Patent No. 644789  
; GENERAL INFORMATION:  
; APPLICANT: LUO, Shun  
; TITLE OF INVENTION: CD16-II VARIANTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,123  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LUO-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-433-123-6

Query Match 7.3%; Score 293; DB 4; Length 233;  
Best Local Similarity 34.7%; Pred. No. 6.3e-18;  
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

Qy 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPO--KTKWY 58  
Db 4 LLLPTALLLVLSAGMRTEPLKAVFLEPQWYRVLEKDSVTLKQCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQGSPLSSPVHLDFFSSASLI 106  
Db 62 HN-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110  
Qy 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPDHPHACILKONGAY 164  
Db 111 LQAPRWVFKEDPHLRCHSWKNTALHKVLYLQNGDKRKYFHNSDPHFKATLKDSGSY 170  
Qy 165 RCTGYKESCCPVSNVKIQVQEPFTRPVLRASSFPISGNPVTLCTETOLSERSDVPL 224  
Db 171 FCRGLVGS-KNVSSETVNITITQGLA--VSTISSFSF-PGVQVSF-CLVMVLLFAVDGTGL 225  
Qy 225 RF 226  
Db 226 YF 227

RESULT 14  
US-08-667-939A-9  
; Sequence 9, Application US/08667939A  
; Patent No. 5998166  
; GENERAL INFORMATION:

APPLICANT: LUO, Shun  
TITLE OF INVENTION: CD16-II VARIANTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/667,939A  
FILING DATE: 24-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/433,123  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LUO-2A  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/433,123  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LUO-2  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-433-123-9  
Query Match 7.3%; Score 292.5; DB 4; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

US-08-667-939A-9  
Query Match 7.3%; Score 292.5; DB 2; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

US-08-433-123-9  
Query Match 7.3%; Score 292.5; DB 4; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

US-08-667-939A-9  
Query Match 7.3%; Score 292.5; DB 2; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

US-08-433-123-9  
Query Match 7.3%; Score 292.5; DB 4; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

US-08-667-939A-9  
Query Match 7.3%; Score 292.5; DB 2; Length 254;  
Best Local Similarity 33.1%; Pred. No. 8e-18;  
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;  
Qy 1 MLLVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58  
Db 4 LLLPTALLLVSAAGRTEDLPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61  
Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLIIQAPLSVF 114  
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118  
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172  
Db 119 KEEDPIHLRCHSWKNWTAHKVTYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178  
Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDD 232  
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223  
Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261  
Db 224 ---GLYFSVKTNIRSTRDKWDHKFKWRK 249

Search completed: May 4, 2005, 11:55:34  
Job time : 27.4304 secs

RESULT 15  
US-08-433-123-9  
Sequence 9, Application US/08433123  
Patent No. 644789  
GENERAL INFORMATION:  
APPLICANT: LUO, Shun  
TITLE OF INVENTION: CD16-II VARIANTS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 80.5296 Seconds  
(without alignments)  
3139.559 Million cell updates/sec

Title: US-09-724-254A-44

Perfect score: 3993

Sequence: 1 MLWVILLVLPVSGQFART.....MVLKVGAEWALPTSSTSEN 759

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3993	100.0	759	15	US-10-057-475B-10460 Sequence 10460, A
3	3993	100.0	759	15	US-10-154-884B-10460 Sequence 10460, A
4	3993	100.0	759	15	US-10-403-847-7 Sequence 7, Appli
5	3993	100.0	759	16	US-10-764-324-10460 Sequence 10460, A
6	3967.5	99.4	790	15	US-10-403-847-4 Sequence 4, Appli
7	3923	98.2	977	14	US-10-040-862-10462 Sequence 10462, A
8	3923	98.2	977	15	US-10-057-475B-10462 Sequence 10462, A
9	3923	98.2	977	15	US-10-154-884B-10462 Sequence 10462, A
10	3923	98.2	977	15	US-10-403-847-9 Sequence 9, Appli
11	3923	98.2	977	16	US-10-764-324-10462 Sequence 10462, A
12	3916	98.1	977	14	US-10-241-220-97 Sequence 97, Appl
13	2962	74.2	592	14	US-10-040-862-10461 Sequence 10461, A

14	2962	74.2	592	15	US-10-057-475B-10461	Sequence 10461, A
15	2962	74.2	592	15	US-10-154-884B-10461	Sequence 10461, A
16	2962	74.2	592	15	US-10-403-847-8	Sequence 8, Appli
17	2962	74.2	592	16	US-10-764-324-10461	Sequence 10461, A
18	1854	46.4	438	15	US-10-403-847-6	Sequence 6, Appli
19	1502	37.6	317	15	US-10-403-847-2	Sequence 2, Appli
20	1419.5	35.5	582	15	US-10-162-335-94	Sequence 94, Appl
21	1417.5	35.5	707	15	US-10-108-260A-4774	Sequence 4774, Ap
22	1417.5	35.5	734	14	US-10-040-862-10463	Sequence 10463, A
23	1417.5	35.5	734	15	US-10-057-475B-10463	Sequence 10463, A
24	1417.5	35.5	734	15	US-10-154-884B-10463	Sequence 10463, A
25	1417.5	35.5	734	16	US-10-764-324-10463	Sequence 10463, A
26	1417.5	35.5	734	17	US-10-948-518-137	Sequence 137, App
27	1400	35.1	727	17	US-10-473-519-20	Sequence 20, Appl
28	1064	26.6	639	16	US-10-408-765A-2410	Sequence 2410, Ap
29	900	22.5	181	16	US-10-363-829-286	Sequence 286, App
30	900	22.5	181	16	US-10-363-829-431	Sequence 431, App
31	884.5	22.2	327	15	US-10-363-616-458	Sequence 458, App
32	871.5	21.8	421	15	US-10-162-335-96	Sequence 96, Appl
33	871.5	21.8	421	15	US-10-162-335-98	Sequence 98, Appl
34	868.5	21.8	508	14	US-10-040-862-10464	Sequence 10464, A
35	868.5	21.8	508	15	US-10-057-475B-10464	Sequence 10464, A
36	868.5	21.8	508	15	US-10-154-884B-10464	Sequence 10464, A
37	868.5	21.8	508	15	US-10-154-884B-11039	Sequence 11039, A
38	868.5	21.8	508	16	US-10-764-324-10464	Sequence 10464, A
39	868.5	21.8	508	17	US-10-948-518-119	Sequence 119, App
40	864.5	21.7	445	15	US-10-154-884B-11043	Sequence 11043, A
41	851.5	21.3	421	15	US-10-162-335-100	Sequence 100, App
42	826.5	20.7	515	14	US-10-040-862-10459	Sequence 10459, A
43	826.5	20.7	515	15	US-10-057-475B-10459	Sequence 10459, A
44	826.5	20.7	515	15	US-10-154-884B-10459	Sequence 10459, A
45	826.5	20.7	515	16	US-10-764-324-10459	Sequence 10459, A

ALIGNMENTS

RESULT 1

- US-10-040-862-10460
- Sequence 10460, Application US/10040862
- Publication No. US20030078396A1
- GENERAL INFORMATION:
- APPLICANT: Gaiger, Alexander
- APPLICANT: Algate, Paul A.
- APPLICANT: Mannion, Jane
- APPLICANT: Retter, Marc
- APPLICANT: Corixa Corporation
- TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
- FILE REFERENCE: 014058-013520US
- CURRENT APPLICATION NUMBER: US/10/040,862
- CURRENT FILING DATE: 2001-11-06
- PRIOR APPLICATION NUMBER: US 60/186,126
- PRIOR FILING DATE: 2000-03-01
- PRIOR APPLICATION NUMBER: US 60/190,479
- PRIOR FILING DATE: 2000-03-17
- PRIOR APPLICATION NUMBER: US 60/200,545
- PRIOR FILING DATE: 2000-04-27
- PRIOR APPLICATION NUMBER: US 60/200,303
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,779
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,999
- PRIOR FILING DATE: 2000-05-01
- PRIOR APPLICATION NUMBER: US 60/202,084
- PRIOR FILING DATE: 2000-05-04
- PRIOR APPLICATION NUMBER: US 60/206,201
- PRIOR FILING DATE: 2000-05-22
- PRIOR APPLICATION NUMBER: US 60/218,950
- PRIOR FILING DATE: 2000-07-14
- PRIOR APPLICATION NUMBER: US 60/222,903
- PRIOR FILING DATE: 2000-08-03
- PRIOR APPLICATION NUMBER: US 60/223,416

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; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-057-475B-10460

Query Match 100.0%; Score 3993; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5e-281;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVQGERVTLTCKGFRFYSPOKTKWYHR 60
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QY 61 YLKGKILRETPDNILVQESGEYRCOAQSPVHLDFSSASLILQAPLSVFEGDSV 120
DB 61 YLKGKILRETPDNILVQESGEYRCOAQSPVHLDFSSASLILQAPLSVFEGDSV 120
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DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPTFRPVLRRASSPQISGNPVTILCTQTLERSDVPFLRFRDDQTLGLWS 240
DB 181 VKIQVEPTFRPVLRRASSPQISGNPVTILCTQTLERSDVPFLRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCTQEDSLRTLYRFYHEGVPLRHKSVRCRGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTILHCTQEDSLRTLYRFYHEGVPLRHKSVRCRGASISFSLTENSNGNYCTADNG 360

; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-057-475B-10460

Query Match 100.0%; Score 3993; DB 14; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5e-281;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVQGERVTLTCKGFRFYSPOKTKWYHR 60
QY 61 YLKGKILRETPDNILVQESGEYRCOAQSPVHLDFSSASLILQAPLSVFEGDSV 120
DB 61 YLKGKILRETPDNILVQESGEYRCOAQSPVHLDFSSASLILQAPLSVFEGDSV 120
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DB 181 VKIQVEPTFRPVLRRASSPQISGNPVTILCTQTLERSDVPFLRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
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DB 301 GTKVTILHCTQEDSLRTLYRFYHEGVPLRHKSVRCRGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLTIVVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLTIVVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
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DB 541 CTADNGFGPQRSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQF 600
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DB 601 YHEDVTLGSSAPSGGSEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGSEASFNLSL 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGSEASFNLSL 720
QY 721 HSGIYSCADNGLRAQSEMTLKVAGEWALPTSTSEN 759
DB 721 HSGIYSCADNGLRAQSEMTLKVAGEWALPTSTSEN 759

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US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
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Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAGKVTLLHCEAQRGSLPILYQPHHDA 420  
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480  
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480  
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEHSGNYY 540  
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEHSGNYY 540  
Qy 541 CTADNGFGPQRSEVSVLFTVTVPSRPILTILVRPRAQAVVGDLLHCEAPRGSPILYWF 600  
Db 541 CTADNGFGPQRSEVSVLFTVTVPSRPILTILVRPRAQAVVGDLLHCEAPRGSPILYWF 600  
Qy 601 YHEDVTLGSSAPSGGGASFNLSLTAHSGNYSCAANNGLVAQHSDTISLTVPVSRPI 660  
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Qy 661 LTPRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTT 720  
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Db 721 HSGIYSCAADNGLEAQRSEMVTLKAVGEWALPTSSTSEN 759

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US-10-154-884B-10460  
; Sequence 10460, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154,884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR FILING DATE: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10460  
; LENGTH: 759  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-154-884B-10460

Query Match 100.0%; Score 3993; DB 15; Length 759;  
Best Local Similarity 100.0%; Pred. No. 6.5e-281;  
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVEFGDSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDTDFHAPHACLKONGAYRCTGYKESCCPVSSNT 180  
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Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPKALNFE 300  
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Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTENGNYCTADNG 360  
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Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAGKVTLLHCEAQRGSLPILYQPHHDA 420  
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAGKVTLLHCEAQRGSLPILYQPHHDA 420  
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480  
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480  
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEHSGNYY 540  
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RESULT 4

US-10-403-847-7  
; Sequence 7, Application US/10403847  
; Publication No. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403,847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR FILING DATE: U.S. 60/368,671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371,420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match      100.0%; Score 3993; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5e-281;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTCKGRPRFFSPQKTWYHR 60
DB      1  MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTCKGRPRFFSPQKTWYHR 60

QY      61  YLGEKILRETPDNLILEVOESGEYRCAQGSPLSSPVHLDFSSASILLQAPLSVFEGDSVV 120
DB      61  YLGEKILRETPDNLILEVOESGEYRCAQGSPLSSPVHLDFSSASILLQAPLSVFEGDSVV 120

QY      121  LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHI PHACLKDNAGYRCTGYKESCCPVSSNT 180
DB      121  LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHI PHACLKDNAGYRCTGYKESCCPVSSNT 180

QY      181  VKIQVQEPFTRPVLIRASSFOPIISGNPVTLTCTETQLSLERSDVPLRFRFRDQDTLGLGWS 240
DB      181  VKIQVQEPFTRPVLIRASSFOPIISGNPVTLTCTETQLSLERSDVPLRFRFRDQDTLGLGWS 240

QY      241  LSPNFOITAMWSKDSGFYCKCAATPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB      241  LSPNFOITAMWSKDSGFYCKCAATPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300

QY      301  GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCBRGASISFSLITTEHSGNYCTADNG 360
DB      301  GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCBRGASISFSLITTEHSGNYCTADNG 360

QY      361  LGAKPSKAVSLISVTVPVSHVNLNLSPPEDILFEGAKVTLHCEAQKSGSLPILYQPFHDEAA 420
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QY      421  LERRSANSAGGVAISFSLTAESHSGNYCTADNGFGPQRKAVSLSTIVPVSHPVLTLSA 480
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QY      481  EALTTFEGATVTLHCEVQRGSQOILYOFVHEMDPLWSSSTPSVGRVSFSLTEGHSNNY 540
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DB      541  CTADNGFGPQRGEVSVSLFTVTPVSRPIILTLRVPAQAVVGDLLLELHCEAPRGSPIILYWF 600

QY      601  YHEDVTILGSSAPSGGEASFNLSLTAESHSGNYSCEANGLVAOHSOTISLSIVLPVSRPI 660
DB      601  YHEDVTILGSSAPSGGEASFNLSLTAESHSGNYSCEANGLVAOHSOTISLSIVLPVSRPI 660

QY      661  LTRAPRAQAVVGDLLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLATTE 720
DB      661  LTRAPRAQAVVGDLLLELHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLATTE 720

QY      721  HSGTYSCEADNGLEAQRSEMTVLKAVGEALPTSTSEN 759
DB      721  HSGTYSCEADNGLEAQRSEMTVLKAVGEALPTSTSEN 759

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RESULT 5  
; Sequence 10460, Application US/10764324  
; Publication No. US20040175739A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Gaiger, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Mannion, Marc

Db 481 EALTFEGATVTLHCEVORGSPQILYQYFHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540  
Qy 541 CTADNGFGPQSRSEVVSFVTPVPSRPILTILRVPRQAQVAVGDLLEHCEAPRGSPPILYWF 600  
Db 541 CTADNGFGPQSRSEVVSFVTPVPSRPILTILRVPRQAQVAVGDLLEHCEAPRGSPPILYWF 600  
Qy 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRP 660  
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRP 660  
Qy 661 LTFRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Db 661 LTFRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720  
Qy 721 HSGIYSCEADNGLEAQRSEMVTLKAVGEWALPTSSTSEN 759  
Db 721 HSGIYSCEADNGLEAQRSEMVTLKAVGEWALPTSSTSEN 759

RESULT 6  
US-10-403-847-4  
; Sequence 4, Application US/10403847  
; Publication No. US20040030098A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN  
; FILE REFERENCE: D0228 NP  
; CURRENT APPLICATION NUMBER: US/10/403,847  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,671  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: U.S. 60/371,420  
; PRIOR FILING DATE: 2002-04-10  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 4  
; LENGTH: 790  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-847-4

Query Match 99.4%; Score 3967.5; DB 15; Length 790;  
Best Local Similarity 96.1%; Pred. No. 4.9e-279;  
Matches 759; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60  
Qy 61 YLGEKILRETPDNLILEVQESGEYRCQAQSGPLSPVHLDFSS----- 102  
Db 61 YLGEKILRETPDNLILEVQESGEYRCQAQSGPLSPVHLDFSSSEMGPPHAAQANVELLGSS 120  
Qy 103 -----ASLIQAPLSVFEQDSVVLRCRAKAEVTLNNTYKNDNLVAFNKR 149  
Db 121 DLLTWSQSAGITASLIQAPLSVFEQDSVVLRCRAKAEVTLNNTYKNDNLVAFNKR 180  
Qy 150 DFHHPHACLDNGAYRGTGKESCCPVSNVTKIQVQEPTRPVLRASSFQPISGNPVTL 209  
Db 181 DFHHPHACLDNGAYRGTGKESCCPVSNVTKIQVQEPTRPVLRASSFQPISGNPVTL 240  
Qy 210 TCETQSLERSDVPLEFRFRDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATWPHSV 269  
Db 241 TCETQSLERSDVPLEFRFRDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATWPHSV 300  
Qy 270 ISDPSRWIQVQIPASHPVLTLSPEKALNFEKTVTLHCETQEDSLRTLYRFYHEGVPLR 329  
Db 301 ISDPSRWIQVQIPASHPVLTLSPEKALNFEKTVTLHCETQEDSLRTLYRFYHEGVPLR 360  
Qy 330 HKSVRCERGASISFSLTTEGNGNYCTADNGLGAKSKAVSLSVTPVPSHPVNLSSPED 389  
Db 361 HKSVRCERGASISFSLTTEGNGNYCTADNGLGAKSKAVSLSVTPVPSHPVNLSSPED 420

Qy 390 LIFEAKVTLHCEAQRGSLPILYQYFHEDALERRRSANSAGGVAISFSLTAHSGNYYCT 449  
Db 421 LIFEAKVTLHCEAQRGSLPILYQYFHEDALERRRSANSAGGVAISFSLTAHSGNYYCT 480  
Qy 450 ADNGFGPQSRKAVSLTSVPSHPVLTLSAEALTFEGATVTLHCEVORGSPQILYQYF 509  
Db 481 ADNGFGPQSRKAVSLTSVPSHPVLTLSAEALTFEGATVTLHCEVORGSPQILYQYF 540  
Qy 510 EDMPWSSSTPSVGRVSFSLTEHSGNYYCTADNGFGPQSRSEVVSFVTPVPSRPILT 569  
Db 541 EDMPWSSSTPSVGRVSFSLTEHSGNYYCTADNGFGPQSRSEVVSFVTPVPSRPILT 600  
Qy 570 LRVPRQAQVAVGDLLEHCEAPRGSPPIYWFYHEDVTLGSSAPSGGASFNLSLTAHSG 629  
Db 601 LRVPRQAQVAVGDLLEHCEAPRGSPPIYWFYHEDVTLGSSAPSGGASFNLSLTAHSG 660  
Qy 630 GNYSCAANGLVAQHSDTISLSVIVPSRPILTFRAPRAQAVVGDLEHCEALRGSSPI 689  
Db 661 GNYSCAANGLVAQHSDTISLSVIVPSRPILTFRAPRAQAVVGDLEHCEALRGSSPI 720  
Qy 690 LYWFYHEDVTLGKISAPSGGASFNLSLTAHSGIYSCEADNGLEAQRSEMVTLKAVGEW 749  
Db 721 LYWFYHEDVTLGKISAPSGGASFNLSLTAHSGIYSCEADNGLEAQRSEMVTLKAVGEW 780

RESULT 7  
US-10-040-862-10462  
; Sequence 10462, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-01352005  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0



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QY 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSNYY 540
DB 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSNYY 540
QY 541 CTADNGFGPORSVSVLFTVPSRPIILTLRVPRQAQAVVGDLLHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPORSVSVLFTVPSRPIILTLRVPRQAQAVVGDLLHCEAPRGSPPILYWF 600
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DB 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660
QY 661 LTRAPRAQAQAVVGDLLHCEALRGSPPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
DB 661 LTRAPRAQAQAVVGDLLHCEALRGSPPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
QY 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746
DB 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746

RESULT 9
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10462

Query Match 98.2%; Score 3923; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 1.1e-275;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTWTFQGERVTLTKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTWTFQGERVTLTKGFRFYSPOKTKWYHR 60
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QY 61 YLQKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSVV 120
DB 61 YLQKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFH1PHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFH1PHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVPVLRFFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVPVLRFFRFRDDQTLGLGWS 240
QY 241 LSNFOITAMWSKDSGFYCKAATMPHSV1SDSPRWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSNFOITAMWSKDSGFYCKAATMPHSV1SDSPRWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCTQEDSLRTLRYFHYHEGVPLRHKSVCERGASISFSLTTTENGNYCTADNG 360
DB 301 GTKVTILHCTQEDSLRTLRYFHYHEGVPLRHKSVCERGASISFSLTTTENGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSTVPSVHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSTVPSVHPVLTLSA 480
QY 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSNYY 540
DB 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSNYY 540
QY 541 CTADNGFGPORSVSVLFTVPSRPIILTLRVPRQAQAVVGDLLHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPORSVSVLFTVPSRPIILTLRVPRQAQAVVGDLLHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPSRPI 660
QY 661 LTRAPRAQAQAVVGDLLHCEALRGSPPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
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DB 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746

RESULT 10
US-10-403-847-9
; Sequence 9, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9
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Query Match 98.2%; Score 3923; DB 15; Length 977;  
Best Local Similarity 100.0%; Pred. No. 1.1e-275;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60

QY 61 YLKEIILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120  
DB 61 YLKEIILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240  
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240

QY 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTILHCEQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360  
DB 301 GTKVTILHCEQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQSGSPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
DB 481 EALTTEGATVTLHCEVQSGSPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGQPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600  
DB 541 CTADNGFGQPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600

QY 601 YHEDVTLGSSAPSGGASFNLSITAEHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 660  
DB 601 YHEDVTLGSSAPSGGASFNLSITAEHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 660

QY 721 HSGIYSCADNGLAQRSEMVTLKVA 746  
DB 721 HSGIYSCADNGLAQRSEMVTLKVA 746

RESULT 11  
US-10-764-324-10462  
; Sequence 10462, Application US/10764324  
; Publication No. US20040175739A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US/10764,324

PRIOR FILING DATE: 2001-11-06  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10467  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10462  
LENGTH: 977  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-764-324-10462

Query Match 98.2%; Score 3923; DB 16; Length 977;  
Best Local Similarity 100.0%; Pred. No. 1.1e-275;  
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60

QY 61 YLKEIILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120  
DB 61 YLKEIILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILQAPLSVFEQDSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240  
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240

QY 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300  
DB 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTILHCEQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360  
DB 301 GTKVTILHCEQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQSGSPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
DB 481 EALTTEGATVTLHCEVQSGSPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGQPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600  
DB 541 CTADNGFGQPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600

QY 601 YHEDVTLGSSAPSGGASFNLSITAEHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 660  
DB 601 YHEDVTLGSSAPSGGASFNLSITAEHSGNYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 660

Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDFISLIVPVSRRPI 660  
Qy 661 LTFRAPRAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
Db 661 LTFRAPRAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746  
Db 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746  
RESULT 12  
US-10-241-220-97  
; Sequence 97, Application US/10241220  
; Publication No. US20030148408A1  
; GENERAL INFORMATION:  
; APPLICANT: Prantz, Gretchen  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Phillips, Heidi  
; APPLICANT: Polakis, Paul  
; APPLICANT: Spencer, Susan  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wu, Thomas  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5010R1-US  
; CURRENT APPLICATION NUMBER: US/10/241,220  
; CURRENT FILING DATE: 2002-12-13  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 97  
; LENGTH: 977  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-241-220-97  
Query Match 98.1%; Score 3916; DB 14; Length 977;  
Best Local Similarity 99.9%; Pred. No. 3.5e-275;  
Matches 745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60  
Qy 61 YLCKEILRETPDNILEVQESGEYRCQAGSPLSPVHLDFSSASLIIQAPLSVFEQDSVV 120  
Db 61 YLCKEILRETPDNILEVQESGEYRCQAGSPLSPVHLDFSSASLIIQAPLSVFEQDSVV 120  
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIPACLKONGAYRCTGYKESCCPVSSNT 180  
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIPACLKONGAYRCTGYKESCCPVSSNT 180  
Qy 181 VKIQVQEPFTRPVLRASSFOPIGPNVTLTCETQLSLERSDVLPRFRFRDDOTLGLGWS 240  
Db 181 VKIQVQEPFTRPVLRASSFOPIGPNVTLTCETQLSLERSDVLPRFRFRDDOTLGLGWS 240  
Qy 241 LSPNFQITAMWSKDSGYWCCKAATPHSVLSDSPRSWIOQVOPASHPVLTLSPEKALNFE 300  
Db 241 LSPNFQITAMWSKDSGYWCCKAATPHSVLSDSPRSWIOQVOPASHPVLTLSPEKALNFE 300  
Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSQNYCTADNG 360  
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTTENSQNYCTADNG 360  
Qy 361 LGAKPSKAVSLSTVPSVSHVPLNLSPEDELIPEGAKVTLHCEAQRSLPLIYQFHEDAA 420  
Db 361 LGAKPSKAVSLSTVPSVSHVPLNLSPEDELIPEGAKVTLHCEAQRSLPLIYQFHEDAA 420  
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSTVPSVSHVPLTLSSA 480  
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSTVPSVSHVPLTLSSA 480

Qy 481 EALTFEAGTATLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSQNY 540  
Db 481 EALTFEAGTATLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSQNY 540  
Qy 541 CTADNGFGPORSEVSLFVTVPSRRPILTLRVPRQAQAVGDLLEHCEAPRGSPILYWF 600  
Db 541 CTADNGFGPORSEVSLFVTVPSRRPILTLRVPRQAQAVGDLLEHCEAPRGSPILYWF 600  
Qy 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDFISLIVPVSRRPI 660  
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDFISLIVPVSRRPI 660  
Qy 661 LTFRAPRAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
Db 661 LTFRAPRAQAVGDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720  
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746  
Db 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746  
RESULT 13  
US-10-040-862-10461  
; Sequence 10461, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10461  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-040-862-10461  
Query Match 74.2%; Score 2962; DB 14; Length 592;  
Best Local Similarity 98.6%; Pred. No. 3e-206;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;



PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10979  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10461  
LENGTH: 592  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-057-475B-10461

Query Match 74.2%; Score 2962; DB 15; Length 592;  
Best Local Similarity 98.6%; Pred. No. 3e-206;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFVSPQKTKWYHR 60  
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFVSPQKTKWYHR 60  
QY 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120  
DB 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240  
DB 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHVPLTILSPEKALNFE 300  
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHVPLTILSPEKALNFE 300  
QY 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
DB 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTPVSHPVLTLSA 480  
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540  
DB 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540  
QY 541 CTADNGFGPQSEVSVLSFVT-----VPVSRPIL 568  
DB 541 CTADNGFGPQSEVSVLSFVTGKCVLASHPPPL 572

RESULT 15  
US-10-154-884B-10461  
Sequence 10461, Application US/10154884B  
Publication No. US2004000561A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Retter, Marc W.  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFVSPQKTKWYHR 60  
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFVSPQKTKWYHR 60  
QY 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120  
DB 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240  
DB 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240  
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHVPLTILSPEKALNFE 300  
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHVPLTILSPEKALNFE 300  
QY 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
DB 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTPVSHPVLTLSA 480  
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTPVSHPVLTLSA 480  
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540  
DB 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540  
QY 541 CTADNGFGPQSEVSVLSFVT-----VPVSRPIL 568  
DB 541 CTADNGFGPQSEVSVLSFVTGKCVLASHPPPL 572

RESULT 14  
US-10-057-475B-10461  
Sequence 10461, Application US/10057475B  
Publication No. US20040002068A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Clapper, Jonathan David  
APPLICANT: Wang, Aijun  
APPLICANT: Ordonez, Nadia  
APPLICANT: Carter, Lauren  
APPLICANT: McNeill, Patricia Dianne  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
TITLE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-014402US  
CURRENT APPLICATION NUMBER: US/10/057,475B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01



;; TITLE OF INVENTION: Hematological Malignancies  
;; FILE REFERENCE: 014058-013521US  
;; CURRENT APPLICATION NUMBER: US/10/154,884B  
;; CURRENT FILING DATE: 2002-05-23  
;; PRIOR APPLICATION NUMBER: US 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: US 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: US 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: US 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: US 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: US 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 11290  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 10461  
;; LENGTH: 592  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-154-884B-10461

Query Match 74.2%; Score 2962; DB 15; Length 592;  
Best Local Similarity 98.6%; Pred. No. 3e-206;  
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;  
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60  
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60  
QY 61 YLGEKILRETPDNLLEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120  
DB 61 YLGEKILRETPDNLLEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120  
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHIPHACLKONGAYRCTGYKESCCPVSSNT 180  
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHIPHACLKONGAYRCTGYKESCCPVSSNT 180  
QY 181 VKIQVEPPTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDQTLGLWS 240  
DB 181 VKIQVEPPTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDQTLGLWS 240  
QY 241 LSPNFQITAMWSKDSGYWCKAATMHSVTSDSRSHIQVQIPASHPVLTLSPKALNFE 300  
DB 241 LSPNFQITAMWSKDSGYWCKAATMHSVTSDSRSHIQVQIPASHPVLTLSPKALNFE 300  
QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360  
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360  
QY 361 LGAKPSKAVSLSVTPVSHVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
DB 361 LGAKPSKAVSLSVTPVSHVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420  
QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVNLSSA 480  
DB 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVNLSSA 480  
QY 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540  
DB 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy 541 CTADNGFGPORSSEVVSFLFTV-----VPVSRPIL 568  
Db 541 CTADNGFGPORSSEVVSFLFTVGTGKCWVLASHPPPL 572  
Search completed: May 4, 2005, 12:01:21  
Job time : 83.5296 secs





RESULT 2

A39878

Fc gamma (IgG) receptor I-A (high affinity) precursor - human

N/Alternate names: CD64

C/Species: Homo sapiens (man)

C/Date: 30-Dec-1991 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004

C/Accession: A39878; I70304; B41357; S03018; I57525

R/van de Winkel, J.G.J.; Ernst, L.K.; Anderson, C.L.; Chiu, I.M.

J. Biol. Chem. 266, 13449-13455, 1991

A/Title: Gene organization of the human high affinity receptor for IgG, Fc gammaRI (CD64)

A/Reference number: A39878; MUID:91302383; PMID:1830050

A/Accession: A39878

A/Molecule type: DNA

A/Residues: 1-374 <VAN>

A/Cross-references: UNIPROT:Q92663; GB:M63830; GB:M63835; NID:g180277; PIDN:AAA35678.1;

R/Porges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.

J. Clin. Invest. 90, 2102-2109, 1992

A/Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.

A/Reference number: I55577; MUID:93055454; PMID:1430234

A/Accession: I70304

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-374 <RES>

A/Cross-references: GB:L03418; NID:gl84840; PIDN:AAA36049.1; PID:g292169

R/Allen, J.M.; Seed, B.

Science 243, 378-381, 1989

A/Title: Isolation and expression of functional high-affinity Fc receptor complementary

A/Reference number: A41357; MUID:89100284; PMID:2911749

A/Accession: B41357

A/Molecule type: mRNA

A/Residues: 1-24, 'S', '26-337, 'T', '339-374 <ALL>

A/Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332

R/Allen, J.M.; Seed, B.

Nucleic Acids Res. 16, 11824, 1988

A/Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR

A/Reference number: S03018; MUID:89098339; PMID:2974947

A/Accession: S03018

A/Molecule type: mRNA

A/Residues: 1-24, 'S', '26-337, 'T', '339-374 <AL2>

A/Cross-references: EMBL:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332

R/Perez, C.; Wietzerbin, J.; Benech, P.D.

Mol. Cell. Biol. 13, 2182-2192, 1993

A/Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma int

ism.

A/Reference number: I57525; MUID:93204964; PMID:8455606

A/Accession: I57525

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-8 <RE2>

A/Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587

C/Genetics:

A/Gene: GDB:FCGR1A; CD64

A/Cross-references: GDB:I35911; OMIM:146760

A/Map position: 1q21-1q21

C/Superfamily: Fc gamma receptor I; immunoglobulin homology

C/Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-292/Domain: extracellular #status predicted <EXT>

F/117-170/Domain: immunoglobulin homology <IMM2>

F/293-313/Domain: transmembrane #status predicted <TM>

F/59, 78, 152, 159, 163, 195, 240/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 10.5%; Score 418.5; DB 1; Length 374;

Best Local Similarity 37.0%; Pred. No. 6.1e-20;

Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;

QY 1 MLLGWILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVLTCTKGFYSPQTKWYHR 60

DB 7 LLLWV-----PVDQ-QVDTTKAVITLQPPVSVFQETVILHCEVLHLPGSSSTQWFLN 59

QY 61 YLIGKEILRETPD---NILEVESGYRQAOGSPVHLDFSASLILCAPLSVF-EG 116

60 --GTATQTSTPSYRIITSSASVNDSEYRCQGLSGRSDPIQLEIHRGMILLQVSRVFTG 117

117 DSVVLACRA-KAEVTLNNTIYKNDVLAFLNKRKTDTHI PHACLKNDNGAYRCTGYKESCCP 175

118 EPALRCHAWKDKLVNVLVYRNGKAFKFFHNSNLTLTKTNISHNGTYHCSGMGKH--R 175

176 VSSNTVKIQOEPPFTRPVLRASSFQ-P-IGNPVTLTCTETSLERSDVPLRFRFRDDQT 234

176 YTSAGISVTVKELFPAPVLNASVTSPLLEGNLVLTSCTLLKLLQRPGLQLYFSYMGSKT 235

235 LGLGWSLSNFOITAMWSKDSGFYWCACAAAMPHSVISDSPSRWIQV--QIP 283

236 L-RGRNTSSYQILTARREDSGLYWCEAATEDGNVLKRSPELEQLVLGLQIP 286

RESULT 3

SH2 domain-containing phosphatase anchor protein 1a - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C:Accession: J07593

F:Xu, M.; Zhao, R.; Zhao, Z.J.

Biochem. Biophys. Res. Commun. 280, 768-775, 2001

A:Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.

A:Reference number: J07593; MUID:21092675; PMID:11162587

A:Accession: J07593

A:Molecule type: mRNA

A:Residues: 1-255 <XUA>

A:Cross-references: UNIPROT:Q9BZ16; GB:AF319438

C:Genetics:

A:Gene: spapla

A:Map position: 1q21

A:Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3

C:Keywords: glycoprotein

F:27-135/Domain: extracellular #status predicted <EXT>

F:68-115/Domain: immunoglobulin-like #status predicted <IG>

F:148-169/Domain: transmembrane region #status predicted <TM>

F:195-255/Domain: intracellular #status predicted <INT>

Query Match 10.1%; Score 405; DB 2; Length 255;

Best Local Similarity 55.2%; Pred No. 2,8e-19;

Matches 95; Conservative 15; Mismatches 38; Indels 24; Gaps 5;

QY 554 VVSLFVTVPVSRPILTLRPRAQAVVGDLELHCEAPRGSPPILYWFYHEDVTLGSSAP 613

DB 35 IAPLCISVPVSRPILTLRSPGAAAVGDLELHCEALRGSPPILYQFYHEDVTLGNSSAP 94

QY 614 SGGEASFNLSTAEHSNGYSCANNGLVAQHSDDTSLSVIVP--VSRPILTLFPRAQAV 671

DB 95 SGGGASFNLSTAEHSNGYSCANNGLGACQSEAVPVISGGDGYRDLMT--AGVWGL 152

QY 672 VGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGASFNLSTLTHSG 723

DB 153 FGVL-----GFTGVALLLYALFH-----KLGES-----SATNEPRG 184

RESULT 4

A46480

Fc gamma (IgG) receptor high affinity - mouse

N:Alternate names: high affinity Igg receptor

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A46480

R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.

J. Immunol. 148, 1570-1575, 1992

A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma

A:Reference number: A46480; MUID:92166399; PMID:1531670

A:Accession: A46480

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-404 <OSM>

A:Cross-references: UNIPROT:P26151

A>Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:8

R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.  
J. Immunol. 144, 371-378, 1990  
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG  
A;Reference number: A43511; MUID:90111035; PMID:2136886  
A;Accession: A43511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-404 <SEA>  
A;Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: immunoglobulin receptor; transmembrane protein  
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 402.5; DB 2; Length 404;  
Best Local Similarity 36.3%; Pred. No. 7.5e-19;  
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY 3 LWVI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60  
DB 10 MWLLTLLLVVPVGGVGNATKAVITLQPPWVIFQKENVTLWCCEGPHLPDSDSTQWFN 69  
QY 61 YLKGKILRETPDNL---EVOEGEYRCQAGSPLSPVHLDFSSASLILQAPLSVF-EG 116  
DB 70 --GTAVQISTPSYSEIPEASQDGEYRCQIGSSWSPDPVOLQIHNWLLQASRRVLTEG 127  
QY 117 DSVVLCRA-KAEVTLNNTIYKNDNVLAFLNKRTHPHACLKONGAYRCTGYKESCCP 175  
DB 128 EPLALRCHGKMKLVNVVYRNGKSFQF--SSDSEVAILKTNLSHGSIYHCSGTGRH--R 184  
QY 176 VSNVTKIQVQEPFTRPVLRASSFQPI-SGNPVTLCETQLSLERSDVPRLRFRFDDQT 234  
DB 185 YTSAGVSIYKELFTTPVLRASSVSSPPFEGSLVTLNCETNLLIQRPLQLHFGFYVGSKI 244  
QY 235 LGLGWSLSPNFQITAMWSKDSGFYCKAATMPSHVSIDSRSWIOVIP-ASHPV 288  
DB 245 LEYR-NTSEYHIAAREDRAGFYWCVEATEDSSVLKRSPELEQLVGLGPOSSAPV 298

RESULT 5  
I48471  
Fc gamma (IgG) receptor high affinity - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I48471  
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Garb  
Science 260, 695-698, 1993  
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig  
A;Reference number: I48471; MUID:93242399; PMID:8480181  
A;Accession: I48471  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-336 <RES>  
A;Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: immunoglobulin receptor  
F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 9.9%; Score 396; DB 2; Length 336;  
Best Local Similarity 36.1%; Pred. No. 1.6e-18;  
Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

QY 3 LWVI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60  
DB 10 MWLLTLLLVVPVGGVGNATKAVITLQPPWVIFQKENVTLWCCEGPHLPDSDSTQWFN 69  
QY 61 YLKGKILRETPD---NILEVOEGEYRCQAGSPLSPVHLDFSSAS-LILQAPLSVF-E 115  
DB 70 --GTAVQISTPSYSEIPEASQDGEYRCQIGSSWSPDPVOLQIHNWLLQASRRVLTE 127  
QY 116 GDSVLCRA-KAEVTLNNTIYKNDNVLAFLNKRTHPHACLKONGAYRCTG---YKE 171  
DB 128 GEPLALRCHGKMKLVNVVYRNGKSFQF--SSGSKIALKTNLSHGSIYHCSGMRHRY 186

QY 172 SCCPVSSNTVKIQVQEPFTRPVLRASSFQPI-SGNPVTLCETQLSLERSDVPRLRFRFPPR 230  
DB 187 TSAGVSI-TVKAPPLLEFTTPVLRASSVSSPPFEGSLVTLNCETNLLIQRPLQLHFGFYV 245  
QY 231 DDQTLGLGWSLSPNFQITAMWSKDSGFYCKAATMPSHVSIDSRSWIOVIP-ASHPV 288  
DB 246 GSKILEYR-NTSEYHIAAREDRAGFYWCVEATEDSSVLKRSPELEQLVGLGPOSSAPV 303

RESULT 6  
A38096  
perlecan precursor - human  
N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate proteoglycan  
C;Species: Homo sapiens (man)  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 12-Jul-2004  
C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736  
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.  
J. Biol. Chem. 267, 8544-8557, 1992  
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membra  
tor, laminin, neural cell adhesion molecules, and epidermal growth factor.  
A;Reference number: A38096; MUID:92235084; PMID:1569102  
A;Accession: A38096  
A;Molecule type: mRNA  
A;Residues: 1-4391 <MUR>  
A;Cross-references: UNIPROT:P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427  
R;Kallunki, P.; Tryggvason, K.  
J. Cell Biol. 116, 559-571, 1992  
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro  
ell adhesion molecules, and epidermal growth factor.  
A;Reference number: A41736; MUID:92112994; PMID:1730768  
A;Accession: S19256  
A;Molecule type: mRNA  
A;Residues: 1-57, 'D', '59-434, 'A', '436, 'FL', '438-449, 'Q', '451-502, 'A', '503-792, 'K', '794-908, 'R',  
71-2979, 'H', '2981-2994, 'G', '2996-3167, 'T', '3169-3240, 'R', '3242-3426, 'R', '3428-3631, 'Q', '3633-363  
A;Cross-references: EMBL:X62515; NID:g29469; PIDN:CAA44373.1; PID:g29470  
R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.  
Genomics 11, 389-396, 1991  
A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the ge  
A;Reference number: A41059; MUID:92120660; PMID:1685141  
A;Accession: A41059  
A;Molecule type: mRNA  
A;Residues: 'RT', '892-908, 'R', '910-1101, 'L', '1103-1132, 'L', '1134-1221, 'L', '1223-1397 <KA2>  
A;Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371  
R;Dodge, G.R.; Kovalevsky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F.  
Genomics 10, 673-680, 1991  
A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular  
A;Reference number: A40306; MUID:91365376; PMID:1679749  
A;Accession: A40306  
A;Molecule type: mRNA  
A;Residues: 1018-1405, 'G', '1407-1409, 'G', '1411-1465 <DOD>  
A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425  
R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den  
J. Cell Biol. 109, 3199-3211, 1989  
A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal  
anas.  
A;Reference number: A33625; MUID:90078352; PMID:2687294  
A;Accession: B33625  
A;Molecule type: protein  
A;Residues: 1379-1384, 'X', '1386-1388, 'X', '1390-1398 <HE2>  
A;Accession: A33625  
A;Molecule type: Protein  
A;Residues: 2166-2171, 'X', '2173-2175, 'X', '2177-2185 <HE3>  
A;Note: peptide potentially matches four different regions of sequence shown  
C;Genetics:  
A;Gene: GDB:HSPG2

A,Cross-references: GDB:126372; OMIM:142461  
A,Map position: lp36.1-lp36.1  
C,Keywords: Chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane  
F,1-21/Domain: signal sequence #status predicted <SIG>  
F,22-4391/Product: perlecan #status predicted <MAT>  
F,22-193/Domain: I <DOM1>  
F,194-530/Domain: II <DOM2>  
F,199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F,285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F,325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F,368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F,531-1676/Domain: III <DOM3>  
F,1159-1206/Domain: laminin-type EGF-like homology <LEG>  
F,1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F,1613-1668/Domain: laminin-type EGF-like homology <LEG>  
F,1677-3686/Domain: IV <DOM4>  
F,2007-2034/Domain: transmembrane #status predicted <TRM>  
F,3687-4391/Domain: V <DOM5>  
F,3845-3880/Domain: EGF homology <EGF1>  
F,3888-3921/Domain: EGF homology <EGF>  
F,3953-4106/Domain: laminin G repeat homology <LG2>  
F,4147-4175/Domain: EGF homology <EGF2>  
F,4149-4151/Region: motor neuron attachment (L-R-E) motif  
F,4299-4301/Region: motor neuron attachment (L-R-E) motif  
F,65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
F,89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval)  
F,2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 9.3%; Score 369.5; DB 2; Length 4391;  
Best Local Similarity 22.9%; Pred. No. 2.5e-15;  
Matches 190; Conservative 118; Mismatches 359; Indels 163; Gaps 39;

Qy 23 PIIFLOPPTVPOGSRVLTCKGFRFYSPQK-TKWHRYLKGKILRETPDNIL-----E 76  
Db 2630 PPIRIESSPTVVEGQTLNLCVVAR--QPQAIITWYKGGSLPSRSHQTHGSLRLHQMS 2687

Qy 77 VOSSGVRQAO-----GSP-----LSSPVHLDPSASLILOAPLSVF 114  
Db 2688 VADSGEYVCRANNIDALEASIVISVPSAGSPSAPGSSMPRIESSSS-----HVA 2739

Qy 115 EGDVSVLRCRAKAEVTLNNTIYKNDVLA--FLNKRTDHIHACLKONGAVRC-----T 167  
Db 2740 EGETLDLNCVPOQAHAQVTHWRGGLSPSHQTRGSRRLRHVSPADSGEYVCRVWGSS 2799

Qy 168 GYKESCCPV--SSNTVKIQVQPFTRPVLR--ASSFQPSGNPVTLC-----ETQLS 216  
Db 2800 GPLEASVLVTIASGSVAHVAPGAPPRIEPPSSRVABGQTLDLKCVPOQAHAQVT 2859

Qy 217 LER--SDVPLRFRFRDDQTLGLGWSLSNFIQTAMWSDKSGFYWCK-----AATMPHSV- 269  
Db 2860 WHKRGGLNPARQVH-----GPLLRLNQVSPADSGEYSCQVTGSGTLEASVL 2907

Qy 270 ISDPSRWIQVQIPASHVPLVLSPEKALNPEGTQVTLHCTQEDSRLTYRFHVEG--VP 327  
Db 2908 VTIEPSSFGIPAPGLAQPTIIEASSHVTGQTLNLCVPOQA--HAQVTWYKGGSLP 2966

Qy 328 LRKSVRCERGASISFSLTT--ENSGNYCYTADNGLGAKPSKAVSLSVTPVSH----- 379  
Db 2967 ARHQT-----HGSQRHLNVPADSGEYVCRASGPG--PQEQASFTVTPPSGSSVRLR 3020

Qy 380 -PVNLSSPDLIFEGAKVTLHCEAQRGSLPIYQFHEDDAALERRSANSAGGVAISFSL 438  
Db 3021 SPVISIDPPSSTVQCGQDASFCKLIHDGAAPISLEWKRTRNOELEDNVHISPNGSIITVG 3080

Qy 439 T-AEHSNGNYCYTADNGLGAKPSKAVSLSVTPVSHVPLVTLSSAEALTFFEGATVTLCEVQ 497  
Db 3081 TRPSNNGTYRCVASNAYGVAQS--VNLNVHSGPPT--VSVLPEGEVWVVKVAVTLEC-VS 3136

Qy 498 RGSPOILYQFVHEDMPILWS--SSTPSVGRVSFSGSLTEGH-----SGNYCYTA 543  
Db 3137 AGEPR-----SSAKRWTRISSTPA-KLBQRTYGLMDSHAVLIQISSAKPSDAGTVYCLA 3187

Qy 544 DNGFGPORSEVSVLFTVTPVSRPILTLRVPRAQAV--GDILLEHCEAPRGSPPILYW-- 599

Db 3188 QNALGTAQKQVEVIVDTGAMAPQVQABEALTVAGHTATLRCSATGSPAPTTHWSK 3247  
Qy 600 -----FYHEDVTLGSSASGGEASNLSTLAHSGNYSCEANGLVAOHS-D-TLSLV 652  
Db 3248 LRSPLPWQHR-----LEGDTLIIPRVAQDQSGYICNATS--PAGHAATILHV 3295

Qy 653 IVPVSRPILTRAPRAQAVVGDLLLEHCEALRGSSPILY-WFYHEDVTLGKISAPSGGGA 711  
Db 3296 ESP---PYATVTPHASVQAGETVQLQCLA-HGTPLPLTFQW-----SRVGSLLPGR 3343

Qy 712 SFNLSL-----TTEHSGIYSCADNGLGAEARSEMVTILKVAGEWALPTSS 755  
Db 3344 TARNELLHFERAAPEDSGRYCRVTKNVKGSAAFAQLLVQGGPGLSPATS 3393

RESULT 7  
138346  
elastic titin - human (fragment)  
C,Species: Homo sapiens (man)  
C,Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C,Accession: 138346  
R,Label: S.; Kolmerer, B.  
Science 270, 293-296, 1995  
A,Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.  
A,Reference number: A57430; MUID:96026330; PMID:7569978  
A,Accession: 138346  
A,Status: preliminary; translated from GB/EMBL/DBJ  
A,Molecule type: mRNA  
A,Residues: 1-7962 <RES>  
A,Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:gl017426; PIDN:CAA62189.1; PID:gl01:  
C,Genetics:  
A,Gene: GDB:TTN  
A,Cross-references: GDB:127867; OMIM:188840  
A,Map position: 2q31-2q31

Query Match 8.7%; Score 347; DB 2; Length 7962;  
Best Local Similarity 24.3%; Pred. No. 1.6e-13;  
Matches 197; Conservative 100; Mismatches 157; Indels 156; Gaps 38;

Qy 23 PIIFLOPPTVPOGSRVLTLC-----KGFRFYSPQKTKWHRYLKGKILRE 69  
Db 216 PTFLSRPKSLTTFVGGAAKFCITVGTVPVETIWKDGAALSPSPNWRISDAENKHILEL 275

Qy 70 TPDNILEVOESGEYRCQAGSPLSPVHLDPSASLIL-----QAPLSVFEQDSVV 120  
Db 276 SN---LTIQDRGVYSCKA-----SNKFGADICQAEELIIDKPHFIKELEPVQSAINKKVH 327

Qy 121 LECRA-----KAEVTLNNTIYK-----NDNVLAFLNKRITDFHIPACLKONGAYRCYTKYES 172  
Db 328 LECQVDEDRKVTVTWWSKDGQKLPQGYKICPEDKIALEIPLAKLKDSGYTVCTASNEA 387

Qy 173 CCPVSNVTVKIQVQPFTRPVLRASSFQPSIGNPVTLTCTQLSLERSDVLRFRRDD 232  
Db 388 GSSSCSAVTVPREPSPFVKV--DPSYLMPLGESARLHCK-----LKGSPV-IQVTFWFKNN 440

Qy 233 QTLGLGWSLSNPF-----QITAMWSDKSGFYWCKAATMPHSHVISDSRSHQVQIOPAS 285  
Db 441 KELSESNTVMYFVNSEAILDITDKVEDSGSYCEAV---NDVGSDDSCSTEIVIKPEPS 497

Qy 286 HPVLTLSPEKALNPEGTQVTLHCT-----OEDSLRT--LYRFYHEGVPLRHK 331  
Db 498 F-IKTELEPADIY--RGTNALLOCEVSGTGPFSEISWFKDKQIRSSKKYRLFQ-----K 548

Qy 332 SVRCERGASISFSLTENSNGNYCYTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLI 391  
Db 549 SLVCLC-----IFSNSADVGEYECVAVNEVGKCGQWATHL-----LKEPPTFVKVKDDLI 599

Qy 392 FEGAKVTLHCEAQRGSLPIL-----YQPHHDAALERRSANSAGGVAISF--SLTAHS 443  
Db 600 ALGGQVTTLQAAVRGSEPISTVMKRGQEVIREDDGKIKMSFSN---GVAVLIIPTDQVQISFG 656

Qy 444 GNYCYTADNGLGAKPSKAVSLSVTPVSHVPLVTLSSAEAL-TFEGATVTLHCEVQRGSPQ 502

Db 657 KYTCLAEENAGSOTSVEILI-----VKPAKIIERAEILQVTAAGDPATLEYTV-AGTPE 710  
Qy 503 ILQYFHEDMPLSSSTPSVGRVSF-----SFLSLEGH-SGNYCTADNGFGPQORSEV 554  
Db 711 LKPKWYKGRPLVASKK--YRISFKNNVAQLKEYSAELHDSGOYTFEISNEVSSSCET 767  
Qy 555 VSLFVTVVPSRPILTTLVRAQAVVGDLELHCEAPRGSPILYFWFHEDVTLGSSAPS 614  
Db 768 TFTVLDRIA-PFTKPLRNVDSVVGTCRLDCKIAGSLPMRVSWF--KD---GKEIAAS 821  
Qy 615 G-----GEASFN-LSLTAESGNYSCAENGLVAQHSDTISLSVIVPSRPILTTRA 665  
Db 822 DRTIAFVEGTASLEIIRVDMNDAGNFTCRATNSVSGKDS-----SGALIVQEPSPVTK 876  
Qy 666 PRAQAVVGDLELHCEALRGSSPT-LYWFYHEDVTLGKISAPSGG-----ASFNL 715  
Db 877 PGSKDVLPGSAVCLKSTFGSTPLTIRWF-----KGNKELVSGGSGYITKEALESLEL 930  
Qy 716 SLT-TEHSGIYSEADN---GLERQORSEMV 741  
Db 931 YLVKTSDSGTYYTCKVSNVAGGVECSANLFV 960

RESULT 8  
S18252  
heparan sulfate proteoglycan - mouse  
N;Alternate names: perlecan  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence,revision 13-Jan-1995 #text\_change 12-Jul-2004  
R;Accession: S18252; A31917; B31917; S66460  
R;Noonan, D.M.; Fullie, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha  
J. Biol. Chem. 266, 22939-22947, 1991  
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog  
adhesion molecule.  
A;Reference number: S18252; MUID:92078153; PMID:1744087  
A;Accession: S18252  
A;Molecule type: mRNA  
A;Residues: 1-3707 <NO>  
A;Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002  
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Ha  
J. Biol. Chem. 263, 16379-16387, 1988  
A;Title: Identification of cDNA clones encoding different domains of the basement membra  
A;Reference number: A92680; MUID:89034110; PMID:2972708  
A;Accession: A31917  
A;Molecule type: mRNA  
A;Residues: 940-1601 <NO2>  
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253  
A;Accession: B31917  
A;Molecule type: mRNA  
A;Residues: 1870-2600 <NO3>  
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301  
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.  
Eur. J. Biochem. 231, 551-556, 1995  
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob  
A;Reference number: S66460; MUID:95377282; PMID:7649154  
A;Accession: S66460  
A;Molecule type: protein  
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>  
C;Keywords: glycoprotein  
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F;764-811/Domain: laminin-type EGF-like homology <LEG>  
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>  
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>  
F;3163-3198/Domain: EGF homology <EGF>  
F;3270-3423/Domain: laminin G repeat homology <LG2>  
F;3464-3482/Domain: EGF homology <EGF7>  
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.4%; Score 336.5; DB 2; Length 3707;  
Best Local Similarity 22.7%; Pred. No. 2.8e-13;  
Matches 190; Conservative 100; Mismatches 365; Indels 183; Gaps 39;  
Qy 23 PIIFLOPPWTTVFGSERVTLTKGFRFYSPQKT-----KWHRVILGKEILRETPDNI 74  
Db 1955 PRVOVGPRTQVHEGRTVRLYCRAGVPSASITWRKEGGSLLPFRHQHGRRLR-----HH 2010  
Qy 75 LEVQESGEYRCQAG-----SPLS-SPVHLDFFSSASLTLOAPLS 112  
Db 2011 MSVADSGEYVCRAANNIDAQETSIMISVSPSTNSPPAPAPIRIESSSS-----R 2062  
Qy 113 VFEGDSVVLRCRAKAEVTLNNTIYKNDNVLAFLNKR--TDFHPHACLKONGAYRC----- 166  
Db 2063 VAEQGTLDLNCVVPFGHAHAQVTHKRGSLPHTHQTHGSRRLRYQVSSADSGEYVCSVLS 2122  
Qy 167 -TCYKESCCPVSSNTVKIQVQEPFTRPVLRL--ASSFQPISGNPVTLTC-----ETQLSL 217  
Db 2123 SSGPLEASVLVSIPTAAANVHIIPGVVPPPIRIETSSSRVABEQTLDSLSCVVPQQAHAQVTW 2182  
Qy 218 ERSDVPLRFRFRDDQTLGLGWSLSPNFI-----TAMWSKDSGFYWCK-----AATMP 266  
Db 2183 HKR-----GGSLPAGHVHGHMLRLNRVSPADSGEYSQVTCSSGTLE 2225  
Qy 267 HSVI-----SDSPRSNIQVQIDA---SHPVLTLSPKALNFEQTKVTLHCETO--EDSLR 316  
Db 2226 ASVLVTIEASEPSP-----IPAGLAQPVYIESSSHLT-EGQTVDLKCVVPGQAHAQ 2277  
Qy 317 TLYRFHEGVPLRHKSVRCERGASIS-FSLTENSNGYCTADNGLGAKSKAVSLSVTV 375  
Db 2278 VTWHKRGSSLPARKHQ-----HGSLLRLYLQSLPADSGEYVQCVAG--SSHEPEHAEFKLTIV 2331  
Qy 376 PVSH-----PVLNLSPEPDLIFEGAKVTLHCEAQGSLPILYOPHHHDAALERRSAN 427  
Db 2332 PSSQNSPRLSRPVSIEPSSSTVQQQODASFCLTHEGAMPKIVKWKIDQLEDNVHI 2391  
Qy 428 SAGGVAISF-----SLTAHSGNYCTADNGFGPQRSKAVSLSTIVPVSHPVLTLSSAEAL 483  
Db 2392 SPNGSIITIVAPGPATMEPTA---CVASNVYGAQS-VVNLSVHGPT--VSVLPEGPVH 2445  
Qy 484 TREGATVTLHCEVQSGPQLLYOFYHEDMPLWSSSTPSVGRVSFSLTSGH----- 535  
Db 2446 VRMGKDTILEC-ISSGEPR-----SSPRMTRLGIPVKLEPRMFGLMNSHAMLKIASV 2496  
Qy 536 ----SGNYCTADNGFGPORSVWSLVF---TPVSRPILTLVRAQAVVGDLELHCE 588  
Db 2497 KPSDAGTYVCOAQNALGTAKQ-VELIVDTGTVPAGTPQVQVESELTEAGTATLHCS 2555  
Qy 589 APRGSPILYFWFHEDVTLGSSAP-----SGGEASPNLSLTAHSGNYSCBANNGLVA 642  
Db 2556 ATGNPPPTIHW-----SKLRAPLPQWHRTEGNTLVIPRVAQDSGGYICNATNS--A 2605  
Qy 643 QHSD-TISLSVIVPSRPILTFRAPRAQAVVGDLELHCEALRGSSPILY-WFYHEDVTL 700  
Db 2606 GHTEATVVLVRESPP--PYATTIPEHTSAQGNLVQLQCLA-HGTPPLTYQW-----SLV 2656  
Qy 701 GKISAPSGGGSFNLISL---TTEHSGIYSCAENGLAEQORSEMVTLLKAVGEMALPTSS 755  
Db 2657 GGVLPEKAVVRNQLRLLEPTVPEDSGRYRCQVSNRVGSAEFAQVLVQSSSNLPDTS 2714

RESULT 9  
I46021  
Fc-gamma receptor II - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 16-Aug-1996 #sequence,revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I46021; S40204  
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.  
Immunogenetics 39, 423-427, 1994  
A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.  
A;Reference number: I46021; MUID:94245284; PMID:8188320  
A;Accession: I46021  
A;Status: preliminary; translated from GB/EMBL/DBJ

RESULT 11  
JH0371





R:Kershaw, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19929  
A:Accession: T24734  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-5198 <W12>  
A:Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b  
A:Experimental source: clone T0999  
C:Genetics:  
A:Gene: him-4; F15G9.4b  
A:Map position: X  
A:Introns: 95/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
; 2512/2; 2933/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;  
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1

Query Match 7.8%; Score 312; DB 2; Length 5198;  
Best Local Similarity 21.6%; Pred. No. 1.7e-11;  
Matches 186; Conservative 123; Mismatches 357; Indels 194; Gaps 43;

QY 14 SQQFARTPRPIIFLOPPWTTVQ-----GERVLTCKGFRFPYSPQTKWHRVYLKGEI 66  
DB 687 AGQ-ARDTDLMLATPPKVEIIQNMVGRGDRVSFECKTIRGKPHKIRNFKN--GKDL 743  
QY 67 LRETPDNILEVOE-----SGEYRCAQ--GSPSSPVHLDPFSSASLILQAPL 111  
DB 744 IK--PDDYKINEGQHINGAKDEAGYSCVGENWAGKDV-QVANLSVGRVPTIIESPH 800  
QY 112 SVFEG--DSVVLRCRA-----KAEV---TLNNTIY---KNDNVLAFLNKRTRDFH 152  
DB 801 TVRVNIERQVTLQCLAVGIPPEIEWQKGNVLLATLNNPRYTQADGNLL----- 850  
QY 153 IPHACLKONGARCTGYKESCCPVSNVTIKIQVEP-----FTRPVLK--ASSQPISG 204  
DB 851 ITDAQIEDQQTCT-----IARTYGOOSQSTTLMTGLVSPFVLGHVPPEQLLEG 901  
QY 205 NPVTLTCTQLSLERSDVLPRFRFRDDOTGLGWSLSPNFOITAMWS-----KDS 255  
DB 902 QDLTSLSCVVLTGTPKPSIV---WIKDDKPVVEG---PTIKIEGGSLRLRGNGPKDE 953  
QY 256 GPYCKAATMPSHVSIDSPSRWIQVQIP-ASHPVLTLSPKALNFEGT-----KVLHC 308  
DB 954 GKYTCTIA-----VSPAGNSTLHINVQLIKKPEFYKPEGGIVFKPTISGDMDEKHAVV 1006  
QY 309 ETQESL-----RTLRFYHGVPLRHKSVRCERGASISFSLTEN----- 349  
DB 1007 NSTHVDLGEFAIPCWSGTPTTITWYLDGRPTPN-----SRDFTVADNTLIV 1058  
QY 350 -----SGNYCTADNGLGAKPSKAVSLSVTPVSHP-VLNLSSPEDLIFEGAKVTLHC 401  
DB 1059 RADKSYSGVYTCQATNSAGDNEQKTTIRIMTPTMISFGSSFNMVVDLF-----TIPC 1113  
QY 402 EAQRGSLPILYOPHHEDAALERSANSAGVAISFSLTAHSGNYYCTADNFGFGORSKA 461  
DB 1114 DVYGDPKVI-TWLLDDKPFTEGVNEDSLTIP-NVNEAHRGTFTTCHQAAG-NDTRT 1170  
QY 462 VSLSIIVPSHPVLTSLSSAALTFEGATVLTACEVQRGSPQILYQFYHEDPMLSSSTPS 521  
DB 1171 VTLTVH-----TTPTINAENQKIALQNDQIVLCECPAKALPPVRLMTY-EGEKIDSLIPH 1226  
QY 522 VGRVSPSFSLTE-----GHSGNYYCTADNFGFGORSSEVSLFVTPV-SRPILTLRVPRAQA 577  
DB 1227 TIREGALVLQNVKLENTGVFVCOVSNLAGE-----SLSYLTIVHEKPIISEVPGVD 1281  
QY 578 VV-GDLELHCAPRGPSPILYKWFYHEDVTLGSSSAPSGGEASFNL-----SLTAE 627  
DB 1282 VVKGFTIEIPCA-TGVPEVIRTWNKNGIDLKMD-----EKKFSVDNLTIRIYEADKN 1334  
QY 628 HSGNYSK-----RANGLVAHQSDTISLSVTPVSRPILTFRAPRAQVAVGDLLELHCEAL 683  
DB 1335 DIGNYNCVVTNEAGTSQMTDVDQBPPIILSTQTNNT-----AVVGDRVELKC-YV 1386  
QY 684 RGSSPILYWFYHEDVTLG---KISAPSGGGSFNLSLTTTSHSGIYSCEADNGL-EAQRSE 739

DB 1387 EASPPASVTWFRGIALGTDTKGYVWESDGLTVIQSASVEDATIVTCKASNPAGKAEANL 1446  
QY 740 MYTLKVAGEWALPTSSSTSEN 759  
DB 1447 QVTIASPDIKDPDVVTQES 1466

RESULT 14  
T42633  
connectin/titin - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
A:Accession: T42633  
R:Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma  
Biochem. Biophys. Res. Commun. 223, 160-164, 1996  
A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re  
A:Reference number: Z22221; MUID:96254045; PMID:8660363  
A:Accession: T42633  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-4162 <YAJ>  
A:Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:gl513029; PIDN:BA11908.1; PID:gl513  
A:Experimental source: breast muscle  
C:Keywords: skeletal muscle

Query Match 7.5%; Score 297.5; DB 2; Length 4162;  
Best Local Similarity 23.2%; Pred. No. 1.1e-10;  
Matches 200; Conservative 113; Mismatches 327; Indels 221; Gaps 51;

QY 5 VILLVLPVSGQFARTPRPIIFLOPPWTTVFGGERVLTCKGFRFYS-----PQ-KTKWY 58  
DB 2956 VLVYNAP-----EPQIIQELQP--TTVBSG-----KPARFCALISGKPOPKVSWY 3000  
QY 59 --HRYLKG---EILRETPDNILEV---QESGEYRCAQGSPLSSPVHLDP-----SSA 103  
DB 3001 KDDQQLSPGFKCFKLHDAQEYTLIIETFPEDSAVYTCEAKN-----DYGVAITSA 3051  
QY 104 SLILQAPLSV-----FEGDSVVLRCRAKAEVTLNNTIYKNDV 141  
DB 3052 SLSVEIPEVPSPELEVYPYPAVIVPLRDATVSEGSARFQCRVTG-TDLKVSWSKORE 3110  
QY 142 L--AFLNKRTRDF-----HIPHACLKONGARCTGYKESCCPVSNVTIKIQVEPFF---- 189  
DB 3111 IKPSRFRMTQFEDTYQLEIAEAYDEGTYTFVNASVGVQVSTAILKLEAPEKIMYEK 3170  
QY 190 -----TRPVLRASSFQPIIS---GNPVLTCETQLSLERSDVLPRFRFRDDQTL- 235  
DB 3171 LEEETEMEVKVAPILR-RRLEPLEVAVNVHAKFTCEVETPN-----VKFOMYKAGREY 3224  
QY 236 -GLGWSL-SPNF---QITAMWSKDSGFYWCKAATMPSHVSIDSPSRWIQVQIPASHPVL 289  
DB 3225 DDKYSIRSSNVLSLEIPRQVVDGCGYSCASQNHGCV---SSTAFLTVTEP----- 3275  
QY 290 TLSPEKALNFEGTKVTLHCETQEDSLR-----TLYRFYHGVPLRHKSVRCERGAS 340  
DB 3276 ---PRFIKLLDSSRLV---KQHDSTRYCKVGGSPKIKVTWYKGETEIHPSK-----YS 3324  
QY 341 ISF-----SLTTNSGNYYCTADNGLGAKPSKAVSLSVTPVVS-----HPVLNLS 385  
DB 3325 MSFVDSVAVLEMHNLISVEDSDGYSCEAQNPAGS-ASTSTSLKVKAPPFTKPPHPVQTL- 3382  
QY 386 SPEDLIFEGAKVTLHCEAQRGSLPILYQFYHEDDAALER-----RSANSAGVAISFSIT 439  
DB 3393 -----KGSVDHLECELO-GTTPPQISWYKDKREIRSSKKYKVMSENVLASIHILNVD 3434  
QY 440 AHSNGNYYCTADNFGFGORSKAVSLSIITVPVSHVPLTSLSSAALTFEGATVTLHCEVQRG 499  
DB 3435 AD-VGEYHCKAVNDVGSD-SCIGSVTLRAP---PTFVKKLSDVTVVVVGETIELQAAVEGA 3489  
QY 500 SP-QILY-----QFYHEDPMLSSSTPSVGRVSPFSFSLTEGHSGNYYCTADNFGFGORS 553  
DB 3490 QPISVLWLKDKGEIITRESENLMISYSENVALSKIG-NAEPTNAGKYICOIKNDAGFQ--- 3545

QY 554 VSLFVTVPSRPIILTLRVP-RAQAVVGDLELHCEAPRSPPI-LYWFYHEDVTLGSSS 611  
Db 3546 --ECFALTVLEPAVIVEKPGVKVTAGDSCTLECTVD-GTPELTARWF----- 3591  
QY 612 APSGGEAS-----FN-----LSLTAHSGNYSCEANGLVAQHSDTISLSVIVP 655  
Db 3592 -KQNEUSTHXYKISFNFKNVKGUKILNAGLEDSGRTTFEVKNS-VGKSCTASLQVSDR 3649  
QY 656 VSRPIILTFRAPRAQAVVGDLELHCEALRGSSPILYWFYH--EDVTLG-KISAP-SGGGA 711  
Db 3650 IMPSPFRKLKETYGLQSSAVLECK-VGSPPIIVSMFHFDGQEITSGDKYQATLTNTC 3708  
QY 712 SFNLS-LTTEHSGIYSCAEN 731  
Db 3709 SLKYNGLQESDMGTYSCTATN 3729

RESULT 15  
A40096  
N:platelet-endothelial cell adhesion molecule-1 (CD31) precursor - human  
P:Alternate names: intercellular adhesion protein, carcinoembryonic antigen; leukocyte a  
C:Species: Homo sapiens (man)  
C:Date: 16-Oct-1992 #sequence revision 16-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: A40096; A48720; J0142; A43536; A40549  
R:Newman, P.J.; Berndt, M.C.; Gorecki, J.; White II, G.C.; Lyman, S.; Paddock, C.; Muller  
Science 247, 1219-1222, 1990  
A:Title: PECAM-1 (CD31) cloning and relation to adhesion molecules of the immunoglobulin  
A:Reference number: A40096; MUID:90193682; PMID:1690453  
A:Accession: A40096  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-738 <NEW>  
A:Cross-references: UNIPROT:P16284; GB:M28526; NID:g189775; PIDN:AAA36429.1; PID:g189776  
A>Note: the nucleic acid sequence is shown in reference A40549  
R:Tang, D.G.; Chen, Y.Q.; Newman, P.J.; Shi, L.; Gao, X.; Diglio, C.A.; Honn, K.V.  
J. Biol. Chem. 268, 22883-22894, 1993  
A:Title: Identification of PECAM-1 in solid tumor cells and its potential involvement in  
A:Reference number: A48720; MUID:94043056; PMID:8226797  
A:Accession: A48720  
A:Molecule type: mRNA  
A:Residues: 507-584 <TAN>  
A:Cross-references: GB:S66450; NID:g435845; PIDN:AAB28645.1; PID:g435846  
A:Experimental source: colon adenocarcinoma  
A>Note: sequence extracted from NCBI backbone (NCBIN:138975, NCBIP:138976)  
R:Simmons, D.L.; Walker, C.; Power, C.; Pigott, R.  
J. Exp. Med. 171, 2147-2152, 1990  
A:Title: Molecular cloning of CD31, a putative intercellular adhesion molecule closely r  
A:Reference number: J0142; MUID:90278365; PMID:2351935  
A:Accession: J0142  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-7, 'ADV', 13-213, 'L', 215-288, 'E', 290-738 <SIM>  
A>Note: the extracellular domain contains four contiguous C2-like immunoglobulin domains  
R:Stocking, H.; Gadd, S.J.; Eher, R.; Majdic, O.; Schreiber, W.; Kasinrerk, W.; Straub  
J. Immunol. 145, 3889-3897, 1990  
A:Title: Molecular characterization and functional analysis of the leukocyte surface pro  
A:Reference number: A43536; MUID:91060975; PMID:1700999  
A:Accession: A43536  
A:Molecule type: mRNA  
A:Residues: 1-124, 'V', 126-562, 'N', 564-669, 'G', 671-738 <STO>  
A:Cross-references: GB:M37780; NID:g187239; PIDN:AAA36186.1; PID:g187240  
R:Albelda, S.M.; Muller, W.A.; Buck, C.A.; Newman, P.J.  
J. Cell Biol. 114, 1059-1068, 1991  
A:Title: Molecular and cellular properties of PECAM-1 (endoCAM/CD31): a novel vascular c  
A:Reference number: A40549; MUID:91340830; PMID:1874786  
A:Contents: annotation  
C:Comment: This protein is a widely distributed glycoprotein on endothelial cells, plate  
A:Gene: GDB:PECAM1  
A:Cross-references: GDB:696372  
A:Map position: 17q23-17q23  
C:Keywords: cell adhesion; glycoprotein; phosphoprotein; transmembrane protein

F;1-27/Domain: signal sequence #status predicted <SIG>  
F;28-738/Product: platelet-endothelial cell adhesion molecule-1 #status predicted <MAT>  
F;340-388/Domain: extracellular #status predicted <EXT>  
F;424-478/Domain: immunoglobulin homology <IMM1>  
F;602-620/Domain: transmembrane #status predicted <TRA>  
F;621-738/Domain: intracellular #status predicted <CYT>  
F;52,84,151,301,320,344,356,453,457,551/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 7.4%; Score 296.5; DB 2; Length 738;  
Best Local Similarity 22.9%; Pred. No. 1.3e-11;  
Matches 136; Conservative 107; Mismatches 251; Indels 101; Gaps 26;

QY 203 SGNPVTLTCTQLSLERSDVPL-RFRFRDQTLGLGWSLSPNFQITAMWSK----- 253  
Db 49 NGKNLTLCQFADVSTTSHVKPQHQMLFYKDDVLF-----YNISSMKSTESYFIPEV 99

QY 254 ---DSGFYNCKAATMPHSVSDSPRSWIVQ-----IPASHPVLTLSPEKALPEGTNYT 305  
Db 100 RIYDSGTIKCTV-----IVNNKEKTAETAYQLLVEGVFS--PRVTLDDKKEAI--QGIVR 149

QY 306 LHCETQEDSLRTLYRFYHGVPLRHKSVCRCGAS-----ISFSLTTEN----- 349  
Db 150 VNCSPVEE--KAPIHTIEKLELNKXVKLKREKNSRDQNFVILEPVEQDVLSPRCQ 207

QY 350 ----SGNYCTADNGIGAKPSKAVSLSVTVVSHPVNLNLSPPEDLIFEGAKVTLHCEAQR 405  
Db 208 ARIISGHHQTSSES-----TKSELVTVTESFSTPKPHI-SPTGMIMEGAQLHKCTIQV 260

QY 406 GSL-----PLIYQFHEDAAL--ERRSANSAGGVAISFSLTAHSGNYYCTADNGFPQR 458  
Db 261 THLAQBFPEIIQO---KDAIIVAHNRHGNKA---VYSVMAMVHESNYTCKVSS---RI 311

QY 459 SKAVSLSITVPVSHPVLTLSAEALTFEGATVTLHCEVQGRSPQILYQFVHEDMPLWSSS 518  
Db 312 SKVSSIVNITELFSKPELESSFTHLDQERLNLSCIP-GAPPANFTIQEDTIV--SQ 368

QY 519 TPSVGRVSFSFSLTEGHSGNYYCTADNGFPQRSEVSLFVTVVPSRPIILTLRVPRAQAV 578  
Db 369 TQDFTKIA-----SKSDSGTYICTAGIDKVKVKSNTVQIVVCEMLSQPRISYDA-QPEVI 422

QY 579 VGDLELHCEAPRGSPPILYWFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANN 638  
Db 423 KGQTIIVRCESISGLTPISYQLLKTSKVLNENSTKNSNDPAVFNKDNPTED--VEYQCVDN 480

QY 639 --GLVAQHSDTISLSVIVPSRPIILTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHE 696  
Db 481 CHSHAKMLSEVLKVKVIAPVDEVOISILSKV-VESGEDIVLQCAVNEGSGPITYKPYRE 539

QY 697 DVTLGKISAPSGGGASF--NLSLTTEHSGIYSC-----EADNGLEAQRSEMVTLKV 745  
Db 540 KEGKPFYQMTSNATQAFWTKQKASKEQEGEYCTAFNRANHASSVPSRKILTVRV 594

Search completed: May 4, 2005, 11:39:26  
Job time : 26.8003 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 102.374 Seconds  
(without alignments)  
3796.562 Million cell updates/sec

Title: US-09-724-254A-44  
Perfect score: 3993  
Sequence: 1 MLLWVILLVLPVSGQFART.....MVLKVGAWALPTSSTSEN 759

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3922	98.2	977	2 Q96RD9	Q96rd9 homo sapien
2	1417.5	35.5	734	2 Q96LA4	Q96la4 homo sapien
3	1417.5	35.5	734	2 Q96P31	Q96p31 homo sapien
4	1417.5	35.5	742	2 Q8NGS2	Q8ngs2 homo sapien
5	1407.5	35.2	740	2 Q96P29	Q96p29 homo sapien
6	1064	26.6	639	2 Q96P30	Q96p30 homo sapien
7	954	23.9	437	2 Q8NF56	Q8nf56 homo sapien
8	927.5	23.2	582	2 Q8OWN2	Q8own2 mus musculus
9	927.5	23.2	595	2 Q68SN8	Q68sn8 mus musculus
10	868.5	21.8	508	2 Q96LA5	Q96la5 homo sapien
11	826.5	20.7	515	2 Q96PJ5	Q96pj5 homo sapien
12	820.5	20.5	515	2 Q96RE0	Q96re0 homo sapien
13	772	19.3	360	2 Q8N732	Q8n732 homo sapien
14	692.5	17.3	508	2 Q8BJA5	Q8bjas mus musculus
15	647	16.2	509	2 Q91YK7	Q91yk7 mus musculus
16	641	16.1	509	2 Q96EY5	Q96ey5 m musman-g pr
17	639	16.0	428	2 Q96PJ6	Q96pj6 homo sapien
18	639	16.0	429	2 Q96LA6	Q96la6 homo sapien
19	628	15.7	366	2 Q8N759	Q8n759 homo sapien
20	548	13.7	124	2 Q6UY46	Q6uy46 homo sapien
21	543.5	13.6	154	2 Q8N733	Q8n733 homo sapien
22	534.5	13.4	422	2 Q96RJ3	Q96rj3 homo sapien
23	481	12.0	722	2 Q6GNB3	Q6gnb3 xenopus lae
24	448.5	11.2	426	2 Q6BAA4	Q6baa4 homo sapien
25	446.5	11.2	626	2 Q6DCH3	Q6dch3 xenopus lae
26	428.5	10.7	357	2 Q8SPW5	Q8spw5 macaca fasc
27	418.5	10.5	374	1 FCGL1 HUMAN	P12314 homo sapien
28	418	10.5	300	2 Q68SF0	Q68sf0 mus musculus
29	418	10.5	324	2 Q7TWH2	Q7tmh2 mus musculus
30	418	10.5	343	2 Q8RAY0	Q8ray0 mus musculus
31	417	10.4	343	2 Q8BYS4	Q8bys4 mus musculus

32	415	10.4	208	2 Q80WN3	Q80wn3 mus musculus
33	405	10.1	255	2 Q9BZ16	Q9bz16 homo sapien
34	402.5	10.1	372	2 Q7YQJ5	Q7yqj5 canis famil
35	402.5	10.1	404	1 FCGL1 MOUSE	P26151 mus musculus
36	401	10.0	144	2 Q9BZ14	Q9bz14 homo sapien
37	401	10.0	192	2 Q9BZ15	Q9bz15 homo sapien
38	396	9.9	330	2 Q8RI42	Q8ri42 mus musculus
39	369.5	9.3	4391	1 PGEM HUMAN	Q98160 homo sapien
40	369	9.2	349	2 Q9MZT0	Q9mzt0 bos taurus
41	360.5	9.0	4071	2 Q6KDZ1	Q6kdz1 gallus gall
42	358.5	9.0	5636	2 Q96RW7	Q96rw7 homo sapien
43	347	8.7	7962	2 Q10465	Q10465 homo sapien
44	347	8.7	34350	2 Q8WZ42	Q8wz42 homo sapien
45	342	8.6	413	2 Q6ZNI1	Q6zni1 homo sapien

ALIGNMENTS

RESULT 1  
Q96RD9 PRELIMINARY; PRT; 977 AA.  
AC Q96RD9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Fc receptor-like protein 5.  
GN Name=FCRH5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;  
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;  
RT "Identification of a family of Fc receptor homologs with preferential  
RT B cell expression.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).  
DR EMBL; AF197453; AAK93971.1; -  
DR HSSP; P12319; 1F2Q.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig; 8.  
DR SMART; SM00408; Igc2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 8.  
KW Receptor.  
SQ SEQUENCE 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;

Query Match	98.2%	Score 3922;	DB 2;	Length 977;
Best Local Similarity	99.9%;	Pred. No. 2.4e-254;		
Matches 745;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60	
Db	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60	
QY	61	YLKKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSASLIQLAPLSVFEQDSVV	120	
Db	61	YLKKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSASLIQLAPLSVFEQDSVV	120	
QY	121	LRCRAEAVTLNNTIYKNDNLVLAFLNKRDTDFH1PHACLKNGAYRCTGYKESCCPVSSNT	180	
Db	121	LRCRAEAVTLNNTIYKNDNLVLAFLNKRDTDFH1PHACLKNGAYRCTGYKESCCPVSSNT	180	
QY	181	VKIQVEPTRPVLIRASSFPISGNPVTLTCTQLSLERSDVPFLRFRFRDDDTLGLGWS	240	
Db	181	VKIQVEPTRPVLIRASSFPISGNPVTLTCTQLSLERSDVPFLRFRFRDDDTLGLGWS	240	
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE	300	
Db	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE	300	



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DR SMART, SM00408; IGc2; 1.
DR PROSITE; PS00835; IG LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 734 AA; 80855 MW; B3411B73A35BC668 CRC64;

Query Match 35.5%; Score 1417.5; DB 2; Length 734;
Best Local Similarity 41.6%; Pred. No. 1.6e-86;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

Qy 1 MLLWVILLVAPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Db 1 MLLWVILLVAPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Qy 60 RYLKKEILRETPDNIIVQSGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Db 60 RYLKKEILRETPDNIIVQSGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Qy 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Db 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTYIKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Db 120 VLRCRAKAEVTLNNTYIKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Qy 117 ILRCQCKNDKNTKQVYKDGKQLPNSYNLEKIVANSVRDNRKSYHCTAYRKFYLDIEV 176
Db 117 ILRCQCKNDKNTKQVYKDGKQLPNSYNLEKIVANSVRDNRKSYHCTAYRKFYLDIEV 176
Qy 177 SNTVXIQVEPEPTRVLRASSFPISGNPVTLCETQLSLERSDVPRLFRFRDDOTLG 236
Db 177 SNTVXIQVEPEPTRVLRASSFPISGNPVTLCETQLSLERSDVPRLFRFRDDOTLG 236
Qy 177 TSKPLNIOVQLFHPVLRASSSTPIEGSPMTLCETQLSPQRPDVLQSLFRDSTGL 236
Db 177 TSKPLNIOVQLFHPVLRASSSTPIEGSPMTLCETQLSPQRPDVLQSLFRDSTGL 236
Qy 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRISWIOVQIPASHPVLTLSPEKA 296
Db 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRISWIOVQIPASHPVLTLSPEKA 296
Qy 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKKSLSQIRVQ----- 281
Db 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKKSLSQIRVQ----- 281
Qy 297 LNPEGTGKTLHCETQSDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Db 297 LNPEGTGKTLHCETQSDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Qy 282 ----- 281
Db 282 ----- 281
Qy 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHH 416
Db 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHH 416
Qy 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAVQSGSTVTFSWHK 324
Db 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAVQSGSTVTFSWHK 324
Qy 417 ED--AALERRSANSAGGVAISFSLTAESHGNYCTADNGFGPQRKQKAVSLSIITVPVSHV 474
Db 417 ED--AALERRSANSAGGVAISFSLTAESHGNYCTADNGFGPQRKQKAVSLSIITVPVSHV 474
Qy 325 EGRVRSLSGRKT-----QRSLLAELH-----V 345
Db 325 EGRVRSLSGRKT-----QRSLLAELH-----V 345
Qy 475 LTLSSAALTFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 475 LTLSSAALTFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEG 534
Qy 346 LTKVESDA----- 353
Db 346 LTKVESDA----- 353
Qy 535 HSGNYCTADNGFGPQRSEVVSFLVTVPSGRPLTLRVPAQAQVGGDLLEHCEAPRGSP 594
Db 535 HSGNYCTADNGFGPQRSEVVSFLVTVPSGRPLTLRVPAQAQVGGDLLEHCEAPRGSP 594
Qy 354 --GRYICADNVHSPILSTWIRTVLPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSP 411
Db 354 --GRYICADNVHSPILSTWIRTVLPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSP 411
Qy 595 PILYFVYHEDVTLGSSAPSGGSEAFNLSTAEHSGNYSCAANNGLVAQHSDTISLVIV 654
Db 595 PILYFVYHEDVTLGSSAPSGGSEAFNLSTAEHSGNYSCAANNGLVAQHSDTISLVIV 654
Qy 412 PILYFVYHEDVTLGSSAPSGGSEAFNLSTAEHSGNYSCAANNGLVAQHSDTISLVIV 471
Db 412 PILYFVYHEDVTLGSSAPSGGSEAFNLSTAEHSGNYSCAANNGLVAQHSDTISLVIV 471
Qy 655 PVSRPILTFAPRAQAQVGGDLLEHCEALRGSPPIYFWFVHEDVTLGKISAPSGGSEAFN 714
Db 655 PVSRPILTFAPRAQAQVGGDLLEHCEALRGSPPIYFWFVHEDVTLGKISAPSGGSEAFN 714
Qy 472 PVSRPILTFAPRAQAQVGGDLLEHCEALRGSPPIYFWFVHEDVTLGKISAPSGGSEAFN 531
Db 472 PVSRPILTFAPRAQAQVGGDLLEHCEALRGSPPIYFWFVHEDVTLGKISAPSGGSEAFN 531
Qy 715 LSLTTHSGNYSCAANNGLVAQHSDTISLVIV 759
Db 715 LSLTTHSGNYSCAANNGLVAQHSDTISLVIV 759
Qy 532 LSLTTHSGNYSCAANNGLVAQHSDTISLVIV 568
Db 532 LSLTTHSGNYSCAANNGLVAQHSDTISLVIV 568

RESULT 4
Q8N6S2
ID Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FCRH3 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
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Db	237	LLGSCGSRSEPHIPAIWTEESRRYQCKAETVNSQVRKQSTAFIIPVQASARFQTHIIP	296
QY	294	EKALNFEQTKVTLHCETOEDSLTLRYFYHEGVP-----LRHKSVRCERGASIS	342
Db	297	ASKLVFEGQLLLNCV-----KGVPGLKFSWYKKOMLNEETKILKSSNAE	343
QY	343	FSLTITTEN---SGNYCTADNGLGAKPSKAVLSVTPVSHVPLNLSPPEDLIFECAKVTIL	399
Db	344	FKISQVNSIDAGEYHCEATNSRRSFVSRAPFITIKVPVSPQVLTJSTGKTQALEGLMVL	403
QY	400	HCEAQRGSLPILYQFHEDDAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRS	459
Db	404	HCOSQRGSPCILYEFPPYENVSLGNSILSGGAYFNFSMSTERSGNYCYCTADNGLGAQCS	463
QY	460	KAVLSLSI-----TVPVS 471	
Db	464	EAIRISIFDMTKNRSVPMA 482	
RESULT 9			
Q68SN8			
ID	Q68SN8	PRELIMINARY; PRT; 595 AA.	
AC	Q68SN8		
DT	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Fc receptor-like protein 3.		
GN	Name=Fch3;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c; TISSUE=Spleen;		
RX	PubMed=15302849;		
RA	Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;		
RA	"Differential B cell expression of mouse Fc receptor homologs.;"		
RL	Int. Immunol. 16:1343-1353 (2004).		
DR	EMBL; AY506558; AAS91578.1; -		
DR	GO; GO:0004872; Fc receptor activity; IEA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG_c2.		
DR	Pfam; PF00047; IG; 3.		
DR	SMART; SM00409; IG; 5.		
DR	SMART; SM00408; IGC2; 4.		
DR	PROSITE; PS50835; IG_LIKE; 5.		
KW	Receptor.		
SQ	SEQUENCE 595 AA; 66619 MW; 6AEBDB8E2F6AFACF CRC64;		
Query Match			
Best Local Similarity 23.2%; Score 927.5; DB 2; Length 595;			
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;			
QY	3	LWVILLVLPVNGQSGARTPRPIIFLQPPWTTVFGERVTLTKCGFRFSPOKTKWYHRYL	62
Db	14	MWLTLLVTPVNGQHEAAQSVSLQPPWTTFFRGEVTLTCYRFGFSVPQTKWYQK--	71
QY	63	GKEILRETPD-----NILEVOESGEYRCQAGSPLSPVHLDFSSASLILOAPLSVFE	116
Db	72	-RKTVKQTPGALIVKANTLKVHESGEYWCQADSLSPSMHVNVEFSEDFVLQAPPVFE	130
QY	117	DSVILRCRAKAVTLNN--TIYKNDVLAFLNKRDTDFHLPACLDKNGAYRCTGVKESC-	173
Db	131	DSVILRCYAKGIEATITFYKDGKALT-LHQSELSIHHANLKDNGQYKCTSKKKWSFG	189
QY	174	CPVSSNTVKIQVEPFRPVLRASSFPQISGNPVTLCETQLSLERSDVLPRFRFRDDQ	233
Db	190	SLYTSNTVGVOVELFPPRLRARSHPIDGSPVLTTCQTLSAQKSDARLQCFERNLQ	249
QY	234	TILGLWSLSPNFQITAMWSKSGFVCKAAATPHSVISDSFSPSIQVQIPASHPVLTISP	293

Db	250	LLGSCGSRSEPHIPAIWTEESRRYQCKAETVNSQVRKQSTAFIIPVQASARFQTHIIP	309
QY	294	EKALNFEQTKVTLHCETOEDSLTLRYFYHEGVP-----LRHKSVRCERGASIS	342
Db	310	ASKLVFEGQLLLNCV-----KGVPGLKFSWYKKOMLNEETKILKSSNAE	356
QY	343	FSLTITTEN---SGNYCTADNGLGAKPSKAVLSVTPVSHVPLNLSPPEDLIFECAKVTIL	399
Db	357	FKISQVNSIDAGEYHCEATNSRRSFVSRAPFITIKVPVSPQVLTJSTGKTQALEGLMVL	416
QY	400	HCEAQRGSLPILYQFHEDDAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRS	459
Db	417	HCOSQRGSPCILYEFPPYENVSLGNSILSGGAYFNFSMSTERSGNYCYCTADNGLGAQCS	476
QY	460	KAVLSLSI-----TVPVS 471	
Db	477	EAIRISIFDMTKNRSVPMA 495	
RESULT 10			
Q96LA5			
ID	Q96LA5	PRELIMINARY; PRT; 508 AA.	
AC	Q96LA5		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Fc receptor-like protein 2 (FCRH2).		
GN	Name=FCRH2; ORFNames=UNQ9236;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;		
RA	Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
RA	"Identification of a family of Fc receptor homologs with preferential		
RT	B cell expression.;"		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.;"		
RL	Genome Res. 13:2265-2270 (2003).		
DR	EMBL; AY043465; AAK91778.1; -		
DR	EMBL; AY358130; AAK88497.1; -		
DR	HSP; P12319; IF2Q.		
DR	Gene; HGNC:14875; SPAP1.		
DR	GO; GO:0004872; Fc receptor activity; IEA.		
DR	InterPro; IPR007110; IG-like.		
DR	Pfam; PF00047; IG; 3.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
KW	Receptor.		
SQ	SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;		
Query Match			
Best Local Similarity 21.8%; Score 868.5; DB 2; Length 508;			
Matches 220; Conservative 60; Mismatches 134; Indels 211; Gaps 12;			
QY	104	SLILOAPLSVFEQGSVVLRCRAKAEVTLNNTYKNDN-VLAFLNKRDTDFHPIHCLKNDG	162

Db 19 SLTLVAPSSVPEGDSIVLKCQGEONWKIQMAYHKONKELSVFKPSDFLIQSAVLSDSG 78  
Qy 163 AYRC-TGYKESCCPVSSNTVKIQVEPFTPLVRASSFQIPISGNPVTLTCTETQLSLERSD 221  
Db 79 NYFCSTKGQLFLMDKTSNI VKIKVQELFQRPVLTASSFQIEGGPVSLKXCETRLSPQLD 138  
Qy 222 VPLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAATMPSHVSIDSPSRWIOVQ 281  
Db 139 VOIQFCFRENOLGSGWSSSPELOISAVWSEDTGYSWCKAETVTHIRKQSLQSQTHVQ 198  
Qy 282 IPASHPVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERGASI 341  
Db 199 ----- 198  
Qy 342 SFSLTENSNGYCTADNGLGAKPSKAVSLVTPVSHPVNLSSPEDLIFEGAKVTLHC 401  
Db 199 -----RIPISNVSLERAPGQVTEQKLLILC 226  
Qy 402 EAORGSLPILYQPHHEDAALERRANSAGVA-ISPSLTAEHSGNYCTADNFGPQORSK 460  
Db 227 SV-----AGGTGNVTFSWYREATG-----TSMGKKTOR 254  
Qy 461 AVLSITVPVSHPVLTLSAEALTPEGATVTLHCEVQSGPOLYQFYHEDMPLWSSSTP 520  
Db 255 SLAELEIP----- 263  
Qy 521 SVGRVSFSLTECHSGNYCTADNFGPQORSVSLFVTPVPSRPILTILTRVPAQAVVG 580  
Db 264 -----AVKESDAGKYCYRADNHVPIQSKVNIPIVPSRPVLTLSRPGAQAVG 314  
Qy 581 DLLELHCEAPRGPPILYWYHEDVTLGSSAPSGGSEAFNLSLTAEHSGNYSCAANNGL 640  
Db 315 DLLELHCEALRGSPPILYQYHEDVTLGNSAPSGGSEAFNLSLTAEHSGNYSCAANNGL 374  
Qy 641 VAQHSITISLVIVP--VSPILTTPAPRAQAVGDLLELHCEALRGSSPILYWFYHEDV 698  
Db 375 GAQCSAVPVISGPGYRDLMT--AGVLWGLFGLV-----GFTGVALLLYALFH--- 423  
Qy 699 TLGKISAPSGGSEAFNLSTLTHSG 723  
Db 424 ---KISGES-----SATNEPG 437

## RESULT 11

Q96PJ5 ID Q96RJ5 PRELIMINARY; PRT; 515 AA.  
AC Q96RJ5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE IFGP2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RX MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;  
RA Guseinikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,  
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;  
RT "A family of highly diverse human and mouse genes structurally links  
RT leukocyte FCg, gp42 and PECAM-1.";  
RL Immunogenetics 54:87-95 (2002).  
DR EMBL; AF329490; AAL23900.1; -;  
DR HSSP; P12319; IF2Q.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
SQ SEQUENCE 515 AA; 57224 MW; F3B7AD14FB1B449A CRC64;

Query Match 20.7%; Score 826.5; DB 2; Length 515;  
Best Local Similarity 43.5%; Pred. No. 4.3e-47;  
Matches 184; Conservative 55; Mismatches 161; Indels 23; Gaps 6;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPOKTKWYHR 60  
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPOKTKWYHR 60  
Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQSGSPVHLDPSSASLILQAPLSVFEQDSV 120  
Db 61 HWYGEKLTLPNTLVRESGLYRCQARGSPRNVLFLSSLSLILQAPYSVEGDTLV 120  
Qy 121 LRCRAKAEVTLNNIYK-NDNVLAFNLKRTDFH PHACLKONGAYRCTGYKESCCPVSSN 179  
Db 121 LRCHRRKEKLTAVKYTWNGNLSISNKGWDLIPQASSNNNGNYRCIGYDENDVPRSN 180  
Qy 180 TVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLW 239  
Db 181 FKIKTQELFPHPELKATDSQPTGNSVNLSCETQLPPERSDTPLFHNFRRDGEVILSDW 240  
Qy 240 SLSPNFQITAMWSKDSGFYWCXAAATMPSHVSIDSPSRWIOVQ-IPASHPVLTLSPEKALN 298  
Db 241 STYPELQLPTVWRENSGSYWCAGETVRGNIHKHSPSLQIHVQRIPIVSGVLTETQPSGQA 300  
Qy 299 FEGTKVTLHCETQEDSLRTLYRFYHGV--PLRHKSVRCERGASISFSLTENSNGNYCT 356  
Db 301 VEGEMLVLCVSAEGTDTTFSWHREDMQESLGRKQTSRLRAELPELPAIRQSHAGGYCT 360  
Qy 357 ANGLGAKSKAVSLVTPVSHPVNLSSPEDLIFEGA-----KVTLHCEAQ 404  
Db 361 ANSYG--PVQSMVLNVTVRETP-----GNRDGLVAAGATGGLLSALLAVALLFHCWRR 413  
Qy 405 RGS 407  
Db 414 RKS 416  
RESULT 12  
Q96RE0 ID Q96RE0 PRELIMINARY; PRT; 515 AA.  
AC Q96RE0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE FC receptor-like protein 4.  
GN Name=FCRH4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;  
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;  
RT "Identification of a family of FC receptor homologs with preferential  
RT B cell expression.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).  
DR EMBL; AF397452; AAK93970.1; -;  
DR HSSP; P12319; IF2Q.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
KW Receptor.  
SQ SEQUENCE 515 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;  
Query Match 20.5%; Score 820.5; DB 2; Length 515;  
Best Local Similarity 43.3%; Pred. No. 1.1e-46;  
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;  
Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGRFYSPOKTKWYHR 60

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Db 1 MLLWASLAPVCGSAAAHKPVISVHPPTWTFKGERVILTCNGQFYATEKTTWYHR 60
QY 61 YLGEILRETPNDILEVQESGEYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
Db 61 HYWGEKLTLPNGNTLEVRSGLYRCQAQGSPPRNVLLFSSDSLILQAPYSVFEQDTLV 120
QY 121 LRCRAAEVTLNNTIYK-NDNVLAFLNKRDTDFHIFACILKNGAYRCTGYKSCCPVSN 179
Db 121 LRCHRRKEKLTAVKYTWNGNLSISNKGWDLILPOASNNNGNYRCIGYGDENDVFRLN 180
QY 180 TVKIQVQEPPTREPLVRASSPQISGNPVTILTCETQLSLERSDVLPRFRFRDDQTLGLCW 239
Db 181 FKILIKIQLFPPHKLATDSQPTGEGSVNLSCETQLPERSDTPLFHNFRRGEVILSDW 240
QY 240 SLSNPNQITAMWSKDSGFYCKAATMPHVSVIDSPRSWIQVQ-IPASHPVLTLSPKALN 298
Db 241 STYPELQLPTVWRENSGSYWCAGAEIVRGNHKSPLQIHVORIPVSGVLLLETQPSGGQA 300
QY 299 FEQTKVTLHCETOEDSLRTLRYFHEGV--PLRHKSVCRCERGASISFSLTTENSQNYCT 356
Db 301 VEGEMLVLCVSAEAGTDTTFSHWREDMQESLGRKTQSLRAELELPALRQSHAGGYCT 360
QY 357 ADNGLGAKPSKAVSLSTVPSVHPVNLSSPEDLIPEGA-----KVTILHCEAQ 404
Db 361 ADNSYG--PVQSMVLNVTRETP-----GNRDLVAAGATGGLSALLAVALLFHWR 413
QY 405 RGS 407
Db 414 RKS 416

RESULT 13
Q8N732 PRELIMINARY; PRT; 360 AA.
AC Q8N732;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DJ801G22.1 (Novel immunoglobulin domain protein similar to
DE immunoglobulin receptors) (Fragment).
GN Name=DJ801G22.1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL135929; CAB92753.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1
FT NON_TER 360
SQ SEQUENCE 360 AA.; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match
Best Local Similarity 46.1%; Score 772; DB 2; Length 360;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIILQEPWTVFQGERVTLTKGFRYSQKWKWHYLGKELLRTPTDNLVEQSG 81
Db 4 KPVISVHPPTWTFKGERVILTCNGQFYATEKTTWYHRHWYGEKLTTPGNTILEVRSG 63
QY 82 EYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVVLRCRAEAEVTLNNTIYK-NDN 140
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Db 64 LYRCQAQGSPPRNVLLFSSDSLILQAPYSVFEQDTLVLRCHRRKEKLTAVKYTWNGN 123
QY 141 VLAFLNKRDTDFHIFACILKNGAYRCTGYKSCCPVSNNTVKIQVQEPPTREPLVRASSFQ 200
Db 124 ILSISNKSWDLLIPQASNNNGNYRCIGYGDENDVFRSNFKIILQIQLFPPHKLATDSQ 183
QY 201 PISGNPVTILTCETQLSLERSDVLPRFRFRDDQTLGLGWSLSPNPQITAMWSKDSGFYWC 260
Db 184 PTEGNSVNLSCETQLPERSDTPLFHNFRRDGEVILSDWSTYPELQLPTVWRENSGSYWC 243
QY 261 KAATMPHVSVIDSPRSWIQVQ-IPASHPVLTLSPKALNFEQTKVTLHCETOEDSLRTL 319
Db 244 GAETVRGNHKSPLQIHVORIPVSGVLLLETQPSGGQAVEGEMLVLCVSAEAGTDTTF 303
QY 320 RPYHEGV--PLRHKSVCRCERGASISFSLTTENSQNYCTADNGLGAKPSKAVSLSTV 375
Db 304 SHWREDMQESLGRKTQSLRAELELPALRQSHAGGYCTADNSYG--PVQSMVLNVT 359

RESULT 14
Q8BJA5 PRELIMINARY; PRT; 508 AA.
AC Q8BJA5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
DE library, clone:FB30015F10 product:weakly similar to SH2 DOMAIN-
DE CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RL sequencing pipeline with 384 multicapillary sequencer.";  
RN Genome Res. 10:1757-1771(2000).  
[6]  
RN SEQUENCE FROM N.A.  
RP STRAIN=NOD; TISSUE=Activated spleen;  
RC STRAIN=NOD; TISSUE=Activated spleen; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; Grouse L.H., Derge J.G.,  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=BALB/c;  
RC STRAIN=BALB/c;  
RX PubMed=15302849;  
RA Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;  
RT "Differential B cell expression of mouse Fc receptor homologs.";  
RL Int. Immunol. 16:1343-1353(2004).  
DR EMBL; BC016551; AAH16551.1; -;  
DR EMBL; AY508556; AAS91576.1; -;  
DR HSSP; Q08380; IBI2.  
DR MGI; MGI:1933397; Msr2.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR Pfam; PF00047; ig; 3.  
DR PRINTS; PR00530; SRCR; 1.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00202; SR; 1.  
DR PROSITE; P550835; IG LIKE; 4.  
DR PROSITE; P500420; SRCR 1; 1.  
DR PROSITE; P550287; SRCR 2; 1.  
KW Receptor.  
SQ SEQUENCE 509 AA; 55757 MW; 25989021E6AF772B CRC64;

Query Match 17.3%; Score 692.5; DB 2; Length 508;  
Best Local Similarity 40.9%; Pred. No. 4.1e-38;  
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;  
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DB 31 LVLPQAPVPEGSVLRCAKAEVTLNN-TIYKNDNLVLAFLNKRDTDFHPLACLKNGQ 90  
QY 164 YRCTGYKESC--CPVSNSTVKIQVPEPFTPLVLRASSFPQISGNVTLTCTETSLERSD 221  
DB 91 YKCTSKKWSFGSLYTSNTVRVQVQLFPPRPLRARPSPHIDGSPVTLTCTQTLQAQSD 150  
QY 222 VPLRFRFRDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAVTHSVISDSRPSVIOVQ 281  
DB 151 ARLOQCFRRQLLGLGSCRSSEFHPAIWTEESKRYQCKAETVNSQVRKQSTAFIPVQ 210  
QY 282 IPASHPVLTLSPEKALNFECTKVTLCETQEDSLRTLRYFYHEGVP-----LRH 330  
DB 211 RASARFQTHIIPASKLVFEGQLLLNCV-----KGVFQPLKFSYWKDMLN 257  
QY 331 KSVRCBERGASISFLTLEN---SGNYCYTADNGLGAKPSKAVSLSVTVPSHPVLMSSP 387  
DB 258 KETKILKSSNAEPKISQVNSIDAGEYHREATNSRRSFVSRAFTITIKVPVSPVLTSTG 317  
QY 388 EDLIFEGAKVTLHCEAQRGLPILYQFHEDALERRSANGAGVAISPLTAHESGNY 447  
DB 318 KTOALEGDLMTLCQSQRGSPFLCYFFYFVNSLGNSSILSGCGAYNFMSRSGNY 377  
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DB 378 CTADNGLGAQCSAIRISIFDMTKNSVPWA 408

RESULT 15  
QY1VK7 PRELIMINARY; PRT; 509 AA.  
AC QY1VK7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Macrophage scavenger receptor 2 (Fc receptor-like protein 2 scavenger isoform).  
GN Name=Msr2; Synonyms=FcRh2;  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
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RC STRAIN=BALB/c;  
RX PubMed=15302849;  
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RT "Differential B cell expression of mouse Fc receptor homologs.";  
RL Int. Immunol. 16:1343-1353(2004).  
DR EMBL; BC016551; AAH16551.1; -;  
DR EMBL; AY508556; AAS91576.1; -;  
DR HSSP; Q08380; IBI2.  
DR MGI; MGI:1933397; Msr2.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR Pfam; PF00047; ig; 3.  
DR PRINTS; PR00530; SRCR; 1.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00202; SR; 1.  
DR PROSITE; P550835; IG LIKE; 4.  
DR PROSITE; P500420; SRCR 1; 1.  
DR PROSITE; P550287; SRCR 2; 1.  
KW Receptor.  
SQ SEQUENCE 509 AA; 55757 MW; 25989021E6AF772B CRC64;

Query Match 16.2%; Score 647; DB 2; Length 509;  
Best Local Similarity 28.0%; Pred. No. 4.6e-35;  
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QY 96 VHLDFSSASLILQAPLSVPEGSVLRCAKAEVTLNNTIYKNDNV-LAFLNKRDTDFHIP 154  
DB 15 VQSDMLSL---PHRSYEGDQVWISCTGKNGDKRLKLYKDKGYHIETSSASSYTR 70  
QY 155 HACLKNDGAYRCYGYKESCCPV-----SSNTVKIQVPEPFTPLVLRASSFPISGNPVLT 210  
DB 71 NARRGDSGYSCKADRKFFLFDITTEETGSKMLNVQELFPAPGLTASLPQVEGSSVTL 130  
QY 211 CETQLSLERSDVPFRFRFRDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAVTHSVI 270  
DB 131 CNTWLPSDRATQLRYSFFKDGHTLQSGWT-SSKFTTSAISKSDSGNYWCENTASRSVS 189  
QY 271 SDSPRSWIQVQ-IPASHPVLTLSPEKALNFECTKVTLCETQEDSLRTLRYFYHEGVP 329

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Db 190 KQSHRSYIDVERIPVSQVTMEIQPSRGWVEG----- 221
QY 330 HKSVRCERGASISFSLTTENSGNYCYCTADNGLCAKPSKAVSLSVTVVSHPVNLNLSSPED 389
Db 222 -----EP 223
QY 390 LIFEKAVTLHCEAQRGSLPILYQPHHEDAALERRRANGSAGGVAISFSLTAHSGNYCYCT 449
Db 224 LVVEGEPLVLACSVAKGTGLITFSHRQD-----TKESVGK----- 259
QY 450 ADNGFGPQSKAVSLITVPVSHPVLTLSAEALTPEGATVTLHCEVQSGPQILYQFYH 509
Db 260 -----KSQRSQVLEIP----- 272
QY 510 EDMPLWSSSTPSVGRVSFSLTEGHSNGNYCYCTADNGFGPQSEVVSFVTVVPSRPILT 569
Db 273 -----TIREGHAGGYCTADNNYGLIOSAIVNITVKIPVNLPLLS 312
QY 570 LRVPRQAQVVGDLLELHCEAPRGSPILYWFYHEDVTLGSSAPSGGEASFNLSLTAHS 629
Db 313 ISVPGVLPFIDGVAELHCEDKRASPPVLYWFYHENITLANTSAFPGKASFKLSTAGHS 372
QY 630 GNYSCAANGLVAQHSOTISLSVIVVPSRPILTFRAPRAQVVGDLLELHCE 681
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